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'note= "framework region
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240
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 62.9
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Aab20359 Anti-chel
Ad920805 Chimeric
Ad92060 Chimeric
Ad73362 Human CD7
Aaw82740 Plasmid p
Aae27925 Human CD7
Aab82834 Antibody
Ad192471 Antibody
Ad192471 Antibody
Ad07028 Anti-HGF
Aab08025 A dimeric
Aao14066 Light cha
Abu08018 Human mon
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1132
1 RSAVVTQESALTTSPGETVT......EVTHQGLSXPVTKSFNRGEC 218
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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Maximum Match 100%
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ADL15445
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Gapop 10.0 , Gapext 0.5
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Add31895 Antibody Add16702 Modified Add79579 Chimeric Aay34096 Parrial a Aay34096 Parrial a Aay34096 Parrial a Aay34096 Parrial a Aay3731 The kappa Aay93731 The kappa Aay93731 The kappa Aay93731 The kappa Aay93791 The Aappa Aay93791 The Aay9806 Dr Aby5483 CJRAOS pr Aby5483 CJRAOS pr Aby5483 CJRAOS pr Aby68491 Hamanised Adb84991 O23 light Aaw06890 Humanised Abr01469 Human ant Ad887940 Anti-IFN-	ALIGNMENTS AA.		chain mutant N96C. ;; CHA255; indium; EDTA; tumour;		n de	. T	0 3
ABJ38595 ADQ31885 ADQ16702 ADP792279 AAY34096 AAX34096 AAX34096 AAX3588 AAX3588 AAX3588 AAX3588 AAX3588 AAX3588 AAX3588 AAX3589 ABJ385 ABJ385 ABJ38 ABJ385 ABJ385 ABJ385 ABJ385 ABJ385 ABJ38 ABJ38 ABJ385 ABJ38	ALIGN		light chelate ein.	alifiers	work work	ement	יב גם ע
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engineering; metal chelate; CHA255; indium; EDTA; tumour;

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(first entry)

"complementarity determining region 1"

38. .52 /label= FR2

note=

"framework region 1"

24. .37 /label= CDR1

ocation/Qualifiers

1. .23 /label= FR1

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Anti-chelate antibody CHA255 light chain.
                                AAB20359 standard; protein; 218
                                                                                                                                                                     cancer; therapy
                                                                                                                                                                                                  Mus musculus.
                                                                                          11-JUN-2001
                                                             AAB20359;
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 RESULT 2
                                                              The invention provides a mutant antibody comprising a reactive site that is not present in the wild-type of the antibody. The antibody also has a complementarity determining region (CDR) that specifically binds to a metal chelate against which the wild-type antibody is raised. The complementarity determining region (CDR) that specifically binds to a within the CDR, such that the chelate antibody are able to form a covalent bond. The present sequence is that of the light chain variable covalent bond. The present sequence is that of the light chain variable covalent bond an example of the method of the livention, rational computer added design was used to develop an indium-EDTPA chelate to covalently compared and the chelate to covalently to chalate in variable of the uncour and then to covalently attach the chalate to the antibody, thereby trapping it at the tumour site. This covalently to chalate to a tumour and then to covalently attach the chalate to the antibody, thereby trapping it at the tumour site. This contains the surface of involved cloning the variable domains of CHA255 to construct a numan/mouse chimeric Fab fragment that could be expressed in Escherichia coll, and the synthesis and screening of benzyl-EDTA chelates carrying veakly electrophilic groups capable of conjugation of the antibody in vivo. This Fab can be conjugated to a targeting moiety when desired. A reactive site was incorporated into the antibody by engineering a Cys residue at location Asn-96 or Ser-95 of the light chain, near the region of the antibody to which the chelate bound. This was accomplished by site anti-chelate antibody anucleic acid encoding the wild-type of the
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99.8%; Score 1130; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 7.4e-80;
Matches 218; Conservative 0; Mismatches 0; Indels 0
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                /note= "encoded by TYG"
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                                                                                                                                       27-SEP-1999; 99US-0156194P.
31-MAY-2000; 2000US-0208684P.
                                                                                                          27-SEP-2000; 2000WO-US026619
                                                                                                                                                                                  (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                 Chmura A;
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Misc-difference 207
                                                                                                                                                                                                                                                            N-PSDB; AAF30633
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Nucleic acid encoding a mutant antibody comprising a reactive site that specifically binds to a metal chelate useful as analytical agents and in clinical diagnosis, as well as in the treatment of disease, particularly
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                                                                                                                                                                                                  /note= "complementarity determining region 3"
                                                               "complementarity determining region 2"
                                                                                                                                                                                                                                                               101. 131
/label= FR4
/note= "framework region 4"
                                                                                                         /label= FR3
/note= "framework region 3"
"framework region 2"
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                                       'label= CDR2
                                                                                                                                                     93. .100
/label= CDR3
                  .59
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complementarity determining region (CDR) that specifically binds to a metal chelate against which the wild-type antibody is raised. The reactive site of the mutant antibody is in a position proximate to or within the CDR, such that the chelate and the antibody are able to form a covalent bond. The present sequence is that of the light chain of antification. The present sequence is that of the light chain of antification. The present sequence is that of the light chain of antification. The present sequence is that of the light chain of antification. The present computer-aided design was used to develop an indium-EDTA chelate to covalently bind to CHA255 in vivo. The premise was to allow the chelate to bind non-covalently to CHA255 bound to a tumour and then to covalently attach the chelate to the antibody, thereby trapping it at the tumour site. This involved cloning the variable domains of CHA255 to construct a human/mouse chimeric Fab fragment that could be expressed in Escherichia coli, and the synthesis and screening of benzyl-EDTA chelates carrying weakly electrophilic groups capable of conjugation of the antibody in vivo. This Fab can be conjugated to a targeting moiety when desired. A reactive site was incorporated into the antibody by engineering a leaf the antibody to which the chelate bound. This was accomplished by site-directed mitagenesis of a nucleic acid arise the region of the antibody to which the chelate bound.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibody engineering; metal chelate; CHA255; indium; EDTA; tumour; cancer; therapy; mutant; mutein.
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98.8%; Score 1118; DB 4; Length 218;
Best Local Similarity 99.5%; Pred. No. 6.4e-79;
Matches 217; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                            encoding the wild-type of the anti-chelate antibody
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/label= CDR2
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/label= FR1
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The invention provides a mutant antibody comprising a reactive site that is not present in the wild-type of the antibody. The antibody also has a complementarity determining region (CDR) that specifically binds to a metal chelate against which the wild-type antibody is raised. The complementarity determining region (CDR) that specifically binds to a conjunct chair which the chelate and the antibody are able to form a covalent bond. The present sequence is that of the light chain variable covalent bond. The present sequence is that of the light chain variable region of anti-indium-EDTA monoclonal antibody CHA255, carrying a S95C mutation. As an example of the method of the invention, rational computer region of anti-indium-EDTA monoclonal antibody CHA255, carrying a S95C covalently to CHA255 bound to a tumour and then to covalently of covalently to CHA255 bound to a tumour and then to covalently to CHA255 bound to a tumour and then to covalently attach the chalate to the antibody, thereby trapping it at the tumour site. This covalent the antibody, thereby trapping is at the tumour site. This coli, and the synthesis and screening of CHA255 to construct a conjugated to a targeting moisery when desired. A reactive site was incorporated into the antibody by engineering a Cys residue at location Ashon96 or Ser-95 of the light chain, near the region of the antibody to which the chelate bound. This was accomplished by site conficed mutagenesis of a nucleic acid encoding the wild-type of the confice antibody.
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                                                                 /label= CDR3
/note= "complementarity determining region 3"
                                                                                                                   note= "replaces Ser of wild-type sequence"
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                               'note= "framework region 3"
                                                                                                                                                                                                          'note= "framework region
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                                                                                                                                                                                                                                                                                 by ACK"
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31-MAY-2000; 2000US-0208684P.
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/label= FR4
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                                                                                                                                                                                                                                                                                                                        'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chmura A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-244971/25.
                                                                                                                                         Misc-difference 100
                                                                                                                                                                                                                               Misc-difference 112
                                                                                                                                                                                                                                                                Misc-difference 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAF30635
                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                           WO200122922-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Meares C,
 Region
                                                     Region
                                                                                                                                                                              Region
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Score 1113; DB 4; Length 218; Pred. No. 1.6e-78;

98.3%; 99.1%;

Query Match Best Local Similarity

'note= "complementarity determining region 2"

Sequence 218 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention relates to multi-functional antibodies that recognise chelating agents and metal chelates, particularly macrocyclic metal chelates. Specifically, it refers to an antibody that comprises a metal chelate bound to an antigen recognition domain, where the metal chelate has a reactive functional group of complementary reactivity to the reactive site of the antibody. This reactive site is the side chain of a naturally occurring amino acid e.g. the -SH group side chain of a cysteine residue (not present in the wild type) which can be used to form a covalent bond between the reactive site of the antibody and the
                                                                                    VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF 120
                                                                                                                       180
                                                                                                                                     61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVF 120
                        9
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                                                                                                                                                                                                                                                                                                                                  Chimeric murine 2D12.5 variable light chain fused to human TTCL protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel mutant antibody comprising reactive site not present in wild-type of antibody and antigen recognition domain that recognizes macrocyclic metal chelate having four nitrogen atoms, useful for treating cancer or
                                      1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG
                       RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG
                                                                                                                      I PPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
                                                                                                                                                                                                                                                                                                                                                        murine; mouse; chimeric; human; TTCL; tetanus toxin; magnetic resonance imaging; lanthanide luminescence; gamma-emissions; single photon emission tomography; SPET; cancer; cytostatic; immunosuppressive; multi-functional antibody; metal chelate; antigen recognition domain; in vivo imaging; cell-antibody-metal chelate complex; emission tomography.
Gaps
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2; Indels
                                                                                                                                                                                      STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                       STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 41; SEQ ID NO 27; 208pp; English.
                                                                                                                                                                                                                                                          ADQ98050 standard; protein; 218 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JAN-2003; 2003US-0035055.
22-JUL-2003; 2003US-00625047.
31-JUL-2003; 2003US-00631259.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-JAN-2004; 2004WO-US001808
                                                                                                                                                                                                                                                                                                          (first entry)
216; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Meares C, Corneillie T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-580725/56.
N-PSDB; ADQ98054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2004065569-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus.
                                                                                                                                                                                                                                                                                                           21-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-AUG-2004.
                                                                                               61
                                                                                                                      121
                                                                                                                                                                       181
                                                                                                                                                                                                                                                                                    ADQ98050;
Matches
                                                                                                                                                                                                                                   RESULT 4
ADQ98050
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               describes using these antibodies for in vivo imaging where the antibody comprises a targeting moiety that binds specifically to a cell via a cell surface receptor or antigen thus forming a cell-autant antibody complex. On addition of the metal chelate, a cell-antibody-metal chelate complex is formed that can be detected using emission tomography, magnetic resonance imaging, lanthanide luminescence, gamma-emissions or single photon emission tomography (SPFT). As such, this method is useful for treating a subject with cancer and pharmaceutical compositions exhibit typotectic and immunosuppressive activities. This polypeptide sequence is the chimeric murine antibody 2D12.5 variable light chain protein fused to the human anti-tetanus toxin antibody kappa light chain constant region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             murine; mouse; chimeric; human; TTCL; tetanus toxin; magnetic resonance imaging; lanthanide luminescence; gamma-emissions; single photon emission tomography; SPET; cancer; cytostatic; immunosuppressive; multi-functional antibody; metal chelate; antigen recognition domain; in vivo imaging; cell-antibody-metal chelate complex; emission tomography; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RSAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGNNNRPPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 VPARFSGSLIGDKAALTIAGTQTEDEAIYFCALWYSNHWVFGGGTKLTVLSRTVAAPSVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RSAVVTQESALTISPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG
reactive functional group of the metal chelate. The present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1079; DB 8; Length 218; Pred. No. 6.8e-76; ); Mismatches 9; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Wild type Asn substituted for Cys"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STLTLSKADYEKHKVYACEVTHQGLSLPVTKSFNRGEC 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2003US-00350555.
2003US-00625047.
2003US-00631258.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.3%;
95.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 95.9
Matches 209; Conservative
                                                                                                                                                                                                                                                                                                                                                         of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 218 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
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Chimeric.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus
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Homo sapiens.

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chelating agents and metal chelates, particularly macrocyclic metal chelates. Specifically, it refers to an antibody that comprises a metal chelates. Specifically, it refers to an antibody that comprises a metal chelate bound to an antigen recognition domain, where the metal chelate che as a reactive functional group of complementary reactivity to the reactive site of the antibody. This reactive site is the side chain of a naturally occurring amino acid e.g. the -SH group side chain of a cysteine residue (not present in the wild type) which can be used to form a covalent bond between the reactive site of the antibody and the cactive functional group of the metal chelate. The present invention describes using these antibodies for in vivo imaging where the antibody complex. On addition of the metal chelate, a cell-mutant antibody complex. On addition of the metal chelate, a cell-mutant antibody complex. Is formed that can be detected using emission tomography, magnetic resonance imaging, lanthanide luminescence, gamma-emissions or single photon emission tomography (SPET). As such, this method is useful for treating a subject with cancer and pharmaceutical compositions exhibit cytostatic and immunosuppressive activities. This polypeptide sequence is the chimeric mutant N33C murine antibody 2D12.5 variable light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VPARFSGSLIGDKAALTIAGTQTEDEAIYFCALWYSNHWVFGGGTKLTVLSRTVAAPSVF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                Novel mutant antibody comprising reactive site not present in wild-type of antibody and antigen recognition domain that recognizes macrocyclic metal chelate having four nitrogen atoms, useful for treating cancer or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to multi-functional antibodies that recognise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, CD72, B-lymphocyte; receptor; scFv; antibody; cytostatic;
immunosuppressive; cancer; autoimmune disease; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'Match 95.2%; Score 1078; DB 8; Length 218; Local Similarity 95.9%; Pred. No. 8.2e-76; les 209; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STLTLSKADYEKHKVYACEVTHOGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                    Claim 41; SEQ ID NO 28; 208pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human CD72-targeted IgG1 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 constant region of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-NOV-2004 (first entry)
(REGC ) UNIV CALIFORNIA
                                                          Meares C, Corneillie
                                                                                                                    WPI; 2004-580725/56.
N-PSDB; ADQ98055.
                                                                                                                                                                                                                                                                                                                          autoimmune diseases.
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Matches
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The present sequence is the protein sequence of the light chain of human CC 1gd1 antibody 025, which specifically recognises human B cell associated antigen CD72. An scFv ADR23124 selected from an antibody phage display library was shown to specifically recognise the human CD72 receptor. The cscw was recloned in IgG expression vector C01 using primars designed to scFv was recloned in IgG expression vector C01 using primars designed to scFv was recloned in IgG expression vector C01 using primars designed to scFv restore complete human frameworks, thereby generating antibody 025. Such anti-CD72 immunosolboulins or their antigen-binding fragments can be used as internalising human binding molecules are capable of (specifically) binding to CD72 or its antigenic determinant, and preferably bind to CD72 caspected with cells. Upon binding to CD72 present on the surface of target cells, the binding molecules internalise. In addition to the internalising human binding molecules, the invention provides of target cells, the binding molecules, the invention provides contrained conjugates comprising an internalising human binding molecule, immunoconjugates or capable of cade encoding these, and compositions comprising them. The internalising human binding molecule, immunoconjugates, nucleic acids encoding these, and compositions comprising them. The molecule or composition can be used in the diagnosis and/or treatment of molecule and B cell associated disorder or disease, especially a B cell associated cancer and B cell associated autoimmune disorder (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                        New internalizing human binding molecules capable of specifically binding to CD72, useful for diagnosing and/or treating B-cell associated diseases, such as cancer or autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARFSGSLIGDKAALTITGAQTEDEARYFCALWYSC--LWVFGGGTKLTVLSRTVAAPSV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 SAVVIQESALITISPGETVILICRSSIGAVITISNYANWVQEKPDHLFTGLIGGINNRAPGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.6%; Score 776; DB 8; 73.5%; Pred. No. 2.4e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 5; SEQ ID NO 54; 174pp; English
                                  Location/Qualifiers
                                                   1. .109
/label= V_region
110. .215
/label= C_region
                                                                                                                                                                                                                              27-JAN-2003; 2003WO-EP050004
                                                                                                                                                                                                                                                                     27-JAN-2003; 2003WO-EP050004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 73.53
Matches 161; Conservative
                                                                                                                                                                                                                                                                                                            (CRUC-) CRUCELL HOLLAND
                                                                                                                                                                                                                                                                                                                                                    Bakker ABH, Marissen
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-580978/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ADR23361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 215 AA;
                                                                                                                                                     WO2004067569-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                    Key
Region
                                                                                             Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is used in a method for obtaining a novel gene construct (A) which expresses, in cells of a mammal, a conjugate (B) of a cell-targeting group (I) and a heterologous prodrug-converting enzyme (II), and (B) is directed to leave the cell for selective localisation at a cell surface antigen (Ag) recognised by (I). Delivery of (A) to a target site, then administration of (III) is used for targeted release of cytocoxic drug, specifically for treating cancer but also inflammation such as rheumatoid arthritis. In situ generation of the targeting antibody increases selectivity, reducing side effects at normal tissue. The method is applicable to any antibody-directed enzyme prodrug therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New gene construct expressing conjugate of targetting agent and prodrug-converting enzyme - useful for, e.g. targetted production of cytotoxic drug in vivo, especially for treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 VVTQESA-LITSPGETVTLICRSSIGAVTISNYANWVQEKPDHLFTGLIGGINNRAPGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VLSQSPAILSASPGEKVTMTCRAS----SSVTYIHWYQQKPGSSPKSWIYATSNLASGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                           Conjugate; cell targeting; cytotoxic drug; prodrug therapy system; prodrug-converting enzyme; cell surface antigen; treatment; cancer; inflammation; rheumatoid arthritis; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                                                                                                                     Plasmid pNG3/A5B7VK-HuCK-NEO protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1f; Page 70; 100pp; English.
AAW82740 standard; protein; 235 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97GB-00009421.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-GB001294
                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 72.2
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blakey DC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-059700/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAV72047.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                   W09851787-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-MAY-1997;
                                                                                                                10-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sc,
                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                        AAW82740;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200
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RESULT

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135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to domain deleted CC49 or C2B8 antibodies. Domain deleted CC49 antibodies comprise a heavy chain human CC49 domain deleted sequence in which CH2 domain has been deleted and are reactive with rumour associated antigen (TAG)-72. The C2B8 antibodies are reactive with CD20 and comprise a heavy chain having a sequence of a derived domain deleted C2B8 construct where the CH2 domain has been deleted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequences of the invention are useful for imaging a neoplasm. They are also useful for treating myelosuppressed patients suffering from neoplastic disorder such as haematologic neoplasm, preferably non-Hodgkin's lymphoma. Autibodies of the invention are also used to treat neoplastic disorder, colon cancer and haematologic malignancy. They are useful for reducing tumour size, inhibiting tumour growth and/or prolonging the survival time of tumour-baring animals and for treating tumours. The present sequence is human C288 light chain protein. This sequence is used in the exemplification of the invention
                                                                                                                                                                    Human, CC49 antibody, C2B8 antibody, tumour associated antigen, TAG-72, neoplasm, neoplastic disorder, haematologic neoplasm, colon cancer, non-Hodgkin's lymphoma, haematologic malignancy, tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 VFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RSAVVTQES--ALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66.7%; Score 755.5; DB 5; 70.5%; Pred. No. 1e-50; ive 16; Mismatches 42;
                                                                                                                                   Human C2B8 antibody light chain protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 3B; 74pp; English.
                     AAE27925 standard; protein; 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chinn
                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-2001; 2001US-0264318P.
16-NOV-2001; 2001US-0331481P.
                                                                                                                                                                                                                                                                                                                                                                 29-JAN-2002; 2002WO-US002373.
                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Braslawsky GR, Hanna N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IDEC-) IDEC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-698547/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 155; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAD45754.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 235 AA;
                                                                                                                                                                                                                                                                                        WO200260955-A2.
                                                                                               27-DEC-2002
                                                                                                                                                                                                                                                                                                                              08-AUG-2002
                                                           AAE27925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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VFIFPPSDEQLKSGTASVVCLLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 12; Fig 31a; 192pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                , Dang W,
Vafa O;
                                                                                                                                       ADL92471 standard; protein; 213
                                                                                                                                                                                                                                                                                                                                                                           27-SEP-2002; 2002US-0414433P.
23-JAN-2003; 2003US-0442301P.
02-MAY-2003; 2003US-0467666F
12-JUN-2003; 2003US-0477839P.
                                                                                                                                                                                                                                                                                                                                                  26-SEP-2003; 2003WO-US030249
                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chirino AJ,
Karki SB, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-316096/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 213 AA;
                                                                                                                                                                                                                                                                                                     WO2004029207-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                         (XENC-) XENCOR
                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                       01-JUL-2004
                                                                                                                                                                                                                                                                                                                             08-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lazar GA,
Hayes RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                 ADL92471;
                                                    179
                                                                            196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
                                                                                                                 RESULT 10
                                                                                                                              ADL9247
                                                                                                                                                     셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a dimeric antibody (1) comprising several

monomeric subunits, where the monomeric subunits are non-covalently
associated. (1) is useful for treating a disorder, especially immune
disorder, and neoplastic disorder such as relapsed Hodgkin's disease,
resistant Hodgkin's disease high grade, low grade and intermediate grade
con-Hodgkin's lymphomas, B cell chronic lymphocytic leukemia (B-CLL),
lymphoplasmacytoid lymphoma (LPL), mantle cell lymphoma (B-CLL),
lymphoma (FL), diffuse large cell lymphoma (DLCL), Burkitt's lymphoma,
clymphoadenopathy, small lymphocytic, follicular, diffuse large cell,
diffuse small oleaved cell, large cell immunoblastic lymphoblastoma,
clieaved and large cell lymphomas, in a mammal (see ABZ24017 for a
cleaved and large cell lymphomas, in a mammal (see ABZ24017 for a
cleaved and large cell lymphomas, in a mammal (see ABZ24017 for a
cleaved and large cell lymphomas, in a mammal (see ABZ24017 for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel dimeric antibody useful for treating immune disorder and neoplastic disorder, has several non-covalently associated monomeric subunits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9/
                                                                                                                                                              C2BB; antibody; cytostatic; antiallergic; antianemic; antiasthmatic; vsotropic; immunomodulator; protozoacide; antidiabetic; nephrotropic; haemostatic; antileprotic; antibacterial; neuroprotective; antipsoriatic; antiheratic; antiarthritic; antiuloer; dermatological; immunosuppressive; antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSAVVTQES--ALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 RGQIVLSQSPAILSASPGEKVTWTCRAS----SSVSYIHWFQQKPGSSPKPWIYATSNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
      LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 755.5; DB 6;
Pred. No. 1e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                    Α,
                                                                                                                                                                                                                                                                                                                                                                                                                     Hariharan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     Д,
                                                                     Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 3B; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       Chinn
                                                                     ABB82834 standard; protein; 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%;
70.5%;
                                                                                                                                                                                                                                                                                                                       29-JAN-2002; 2002WO-US002374.
                                                                                                                                                                                                                                                                                                                                            29-JAN-2001; 2001US-0264318P.
16-NOV-2001; 2001US-0331481P.
21-DEC-2001; 2001US-0341858P.
                                                                                                                                            Antibody C2B8 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     Braslawsky GR, Hanna N,
                                                                                                                                                                                                                                                                                                                                                                                              (IDEC-) IDEC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-140446/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 155; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABZ24018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 235 AA;
                                                                                                                                                                                                                                                                      WO200296948-A2
                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                    31-MAR-2003
                                                                                                                                                                                                                                                                                              05-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
         196
                                                                                             ABB82834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loc
Matches
                                              RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
cytostatic; antiinflammatory; cardiovascular; gene therapy; antibody; Fc; agriculture; industrial application.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an antibody comprising an Fc variant portion having an amino acid modification in the Fc region of the parent Fc polypeptide, where the Fc variant modulates binding to an Fc-gamma-R compared to the parent Fc polypeptide. The antibody may also be used in research and in agricultural or industrial applications. This sequence corresponds to the light chain of the antibody "Rituximab" as an example of an antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New optimized Fc variant antibody useful for diagnosing or treating diseases (e.g. cancer, inflammation or cardiovascular diseases), in research and in agricultural or industrial applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Doberstein SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39; Indels
                                                                                   LSSTLTLSKADYEKHKVYACEVTHOGLSXPVTKSFNRGEC 218
                                                                                                                    Desjarlais JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.7%; Score 755; DB 8; 71.8%; Pred. No. 1e-50; iive 16; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antibody "Rituximab" light chain sequence.
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(revised)
(first entry)

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AAB08025 standard, protein, 235 AA.
                                                                                                                                                                                                                                                                                                                                                                                     28-JAN-1999;
                                                         12-SEP-2003
14-NOV-2000
                                                                                                                                                                                                                                                                                                                                              03-AUG-2000
                                      AAB08025;
                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                               Protein
          AAB08025
                    ,;
(7
                                                                                                                                                                                                                                                                                                                                                                                                                5DS Fab comprises a light chain (AAW07528) and heavy chain (AAW07529) of monoclonal antibody (WAb) 5DS, a murine MAb raised against the hepatocyte growth factor (HGF) receptor (c-Met). The Fab can be obtd. by papain digestion of the MAb or by recombinant methods utilising cDNA clones (AAT43873-74) coding for the light and heavy chains. 5DS Fab is an antagonist of the HGF receptor and is useful for the diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEQLKSGTASUVCLIANFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSTLTL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89
                                                                                                                                                                                                                                                                                                                                                      Hepatocyte growth factor receptor antagonist - specifically anti-c-Met receptor monoclonal antibody 5D5 Fab, useful for mammalian cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:|| | || || :|:|| || SSLTVSVGEKVTVSCKSSQSLLYTSSQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SALTISPGETVTLICRSSIGAVTIS --- NYANWVQEKPDHLFTGLIGGINNRAPGVPARF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIFPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4,
                                                                                                                                              Hepatocyte growth factor receptor; HGF; c-Met, antagonist, monoclonal antibody; MAb; Fab; breast cancer; pancreas cancer; colon cancer; lung cancer; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment of breast, pancreas, colon and lung cancer
           LTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66.3%; Score 751; DB 2; 71.8%; Pred. No. 2.1e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Mismatches
                                                                                                                             Anti-HGF receptor MAb 5D5 Fab light chain.
                                                                  AAW07528 standard; protein; 220 AA
                                                                                                                                                                                                                                                                                                                                                                                              Claim 12; Fig 1A; 69pp; English.
                                                                                                                                                                                                                                                96WO-US008094.
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                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                        Tabor KH;
                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                            WPI; 1997-034371/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT43873.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 220 AA;
                                                                                                                                                                                                         WO9638557-A1
                                                                                                                                                                                                                                              31-MAY-1996;
                                                                                                                                                                                                                                                                 02-JUN-1995;
                                                                                                        04-MAR-1997
                                                                                                                                                                                                                            05-DEC-1996.
                                                                                                                                                                                                                                                                                                        Schwall RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 153;
                                                                                                                                                                                                                                                                                                                                                                            treatment.
                  178
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183
                                                                                      AAW07528;
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                                                RESULT 11
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The present sequence represents a dimeric anti-CD20 light chain

CC polypeptide. The dimeric immunoglobulin is used in the method of the
polypeptide. The dimeric immunoglobulin is used in the method of the

CC invention. The specification describes a method for producing an
immunoglobulin (1g) G/1gG dimer. The method comprises genetically
cengineering a monoclonal antibody to introduce a cysteine molecule which
inhibite formation of intramolecular disulphide bridges between sister
heavy chains on the same antibody molecule. The dimer is a homodimer or
thererodimer that is capable of activating components of the complement
cascade. The dimer is also capable of binding to Fegamma receptors on

Cyctotoxic effector cells and on host immune cells, and is capable of
initiating programmed cell death. The IgG/IgG dimers may be used to treat
allergic disorders, cancers and autoimmune diseases such as allergic
athma, allergic bronchopulmonary aspergillosis, allergic thinitis,
cathma, allergic contact dermatitis, Crohn's disease, Graves's disease, food allergies,
callergic contact dermatitis, CLL cancers and/or B-cell lymphomas. They
may also be used to treat a range of other diseases and disorders such as
rhemmatoid arthritis, leprosy, Lyme disease, diabetes mellitus, candidiasis
                                                                  Anti-CD20 antibody; dimeric immunoglobulin; immunoglobulin; IgG; complement system; Fcgamma receptor; cytotoxic effector cell; host immune cell; allergic disorder; cancer; autoimmune disease; allergic asthma; atopic dermatitis; Crohn's disease; allergic bronchopulmonary aspergillosis; allergic rhinitis; Graves's disease; food allergy; allergic contact dermatitis; cancer; B-cell lymphoma; rheumatoid arthritis; ulcerative colitis; psoriasis; pigeon breeder's disease; hopatitis; leprosy; Lyme disease; disease; aplastic anaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetically engineering immunoglobulin (Ig) G/IgG dimers for the treatment of cancers, allergic disorders and autoimmune conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129. .235
/note= "human kappa light chain constant region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Braslawsky GR, Hanna N, Hariharan K, Labarre MJ, Huynh TB;
A dimeric anti-CD20 light chain polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Fig 1A-B; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-00238741.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JAN-2000; 2000WO-US001893.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IDEC-) IDEC PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000-514811/46.
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Homo sapiens.
Chimeric.
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useful
spread
                                                                                                                         ω,
and aplastic anaemia. They are also useful for inducing hyper-cross-linking of membrane antigens and for the preferential killing of selected cell populations. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                    118
                                                                                                                                                                                                                                                                                                                 195
                                                                                                                                                                                                                                                   135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the light chain protein of the monoclonal antibody from clone JA. The invention relates to an isolated human monoclonal rabies virus neutralising antibody (virucide) derived from cDNA clones encoding the antibody heavy and light chains expressed in heterologous expressed on systems and purified away from deleterious contaminants. The invention provides a fused gene encoding a chimeric immunoglobulin light chain and a fused gene encoding a chimeric immunoglobulin heavy chain. The antibody of the invention is useful for treating an individual exposed to a rabies virus by administering to the
                                                                                                                                                                                                                                                                                119 VFIFPPSDEQLKSGTASVVCLLANNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human rabies-immune globulin; monoclonal; virucide; heavy chain; monoclonal rabies virus neutralising antibody; immunoglobulin; chain; central nervous system; CNS; prophylactic therapy; clone JA.
                                                                                                                                                        28
                                                                                                                                                                                     96
                                                                                                                                                                                                                   59 PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPS
                                                                                                                                                                                                                                                                                                    VET PPPSDEOLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTVS
                                                                                                                                                                                                                                         1 RSAVVTQES--ALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRA
                                                                                                                                                                          21 RGQIVLSQSPAILSASPGEKVTMTCRAS----SSVSYIHWFQQKPGSSPKRWIYATSNLA
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated human monoclonal rabies virus neutralizing antibody for treating individual exposed to rabies virus and for preventing of rabies virus to central nervous system.
                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Light chain protein of the monoclonal antibody from clone JA.
                                                                                              Length 235;
                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                 LSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                           43;
                                                                                              DB 3;
                                                                                            Score 750.5; DB 3
Pred. No. 2.5e-50;
                                                                                                                           16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 24-25; 25pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAO14066 standard; protein; 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYJE-) UNIV JEFFERSON THOMAS
                                                                                          66.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAY-2000; 2000US-0204518P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-MAY-2001; 2001WO-US014468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                             154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dietzschold
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N-PSDB; AAK98702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
                                                                                               Query Match
Best Local Similarity
                                                                  Seguence 235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200188132-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA014066;
                                                                                                                                                                                                                                                     11
                                                                                                                                                                                                                                                                                                                    136
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                                                                                                                                                                                                                                                                                                                                                                                196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HRIG;
                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                               AA014066
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individual a therapeutically effective amount of the antibody, and preventing a spread of the rabies virus to the central nervous system (CNS). The antibody of the invention provides a safe and efficacious post-exposure prophylactic therapy for individuals exposed to a rabies virus
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                                                                                                                                                                                                                                                                                    182
                                                                                                                                                                                                                                                                                                        The invention discloses a recombinant antibody comprising a constant region of monoclonal antibody (Mab) 57 linked to a non-Mab 57 variable region. Rabies is an acute, neurological disease caused by infection of the central nervous system with the rabies virus, a member of the Lyssavirus genus of the family Rhabdoviridae. Also disclosed are methods for producing an isolated recombinant antibody by culturing a host cell, containing a recombinant expression vector comprising the nucleic acid
                                                                                                                                                                 62
                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant antibody comprising a constant region of Mab 57 linked t
a non-Mab 57 variable region, useful for treating an individual exposed
to a pathogen, e.g. rabies infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human monoclonal rabies virus antibody light chain, clone JH, protein.
                                                                                                                                                                                  PPSDEQLKSGTASVVCLLINNFYPREAKVOWKVDNALQSGNSQESVTEQDSKDSTYSLSST
                                                                                                                                                                                                                          ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF
                                                                                                                                                                 4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, antibody, constant region, monoclonal antibody 57, Mab 57 variable region; Rabies, neurological disease; infection; central nervous system; rabies virus; Lyssavirus; Rhabdoviridae; pathogen; vaccine; virucide; light chain.
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2
                                                                                                      Length 234;
                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                218
                                                                                                      Score 749.5; DB 5;
Pred. No. 3e-50;
3; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                            234
                                                                                                                                                                                                                                                                                                                                                                 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 33-34; 38pp; English
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                                                                                                      66.2%; Scor
71.8%; Pred
tive 13; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU08018 standard; protein; 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-AUG-2002; 2002WO-US026584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-AUG-2001; 2001US-0314023P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                         Best Local Similarity /1.8
Matches 155; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dietzschold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-278566/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABX12856
                                                                               Sequence 234 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003016501-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                           80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABU08018;
                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                        123
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molecule encoding the antibody, and isolating the recombinant antibody expressed and treating an individual exposed to a pathogen by administering to the individual the recombinant antibody. The recombinant antibodies are useful for preventing (vaccine) and treating an individual exposed to a pathogen, e.g. rabies infection. They are also useful for the qualitative and quantitative determination of the rabies virus. The sequences presented are the antibody protein fragments, the nucleic acids encoding them or the PCR primers used to construct the recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                       PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 198
                                                                                                                                                                                                                                                                                                                                   ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
                                                                                                                                                                                                                                                                                                                                                                    ARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQGTKVE-FKRTVAAPSVFIF 138
                                                                                                                                                                                                                                                                                                 VLTOSPATISISPGERATLACRAS---QTASRYLAWYOOKPGQAPRILIYDTSNRATGIP 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid molecule encoding a sequence that neutralizes an antibody that binds to rables virus protein, useful for diagnosing, preventing or treating infection of pathogens that target neuronal tissues, e.g. rables.
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monoclonal rabies virus neutralising antibody; rabies virus protein;
neuronal tissue; antirabies.
                                                                                                                                                                                                                                    5.
                                                                                                                                                                                                  Length 234;
                                                                                                                                                                                                                                    43; Indels
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                                                                                                                                                                                                  Score 749.5; DB Pred. No. 3e-50;
                                                                                                                                                                                                                                   13; Mismatches
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04-MAY-2001; 2001US-00848832.
21-AUG-2001; 2001US-0314023P.
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71.8%;
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N-PSDB; ADF65790.
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DIETZSCHOLD
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Best Local Similarity
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                                                                                                                                                                     Sequence 234 AA;
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Claim 2; SEQ ID NO 4; 22pp; English

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122
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        The present invention relates to the isolation of immunoglobulin (Ig) heavy and light chains of human monoclonal rabies virus neutralising antibody, and the polynucleotide sequences encoding them. The antibody specifically binds to a rabies virus protein. Also disclosed is a fused gene encoding a chimeric immunoglobulin light or heavy chain comprising itset DNA sequence encoding an immunoglobulin light or heavy chain variable region of a monoclonal rabies virus neutralising antibody produced by a heterohybridoma cell line and a second DNA sequence encoding a recombinant antibody. The polynucleotide sequences and methods are useful for diagnosing, preventing or treating antibodies and methods are useful for diagnosing, preventing or treating an infection of pathogens that target neuronal tissues, particularly reading.
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7, 2005, 15:54:03 ch completed: June time: 117.5 secs Search

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Sequence 1, Ag
Sequence 1, Ag
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.: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-669-971-1

US-09-472-087-67

US-09-472-087-67

US-09-011-769A-27

US-08-315-926A-79

US-09-472-087-14

US-09-472-087-14

US-09-472-087-14

US-09-472-087-14

US-09-472-087-65

US-09-453-234-46

US-09-453-234-46

US-09-456-090A-36

US-09-456-090A-36
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Maximum Match 100%
Listing first 45 summaries
                                                                                         protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                              seq length: 0
seq length: 200000000
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1132
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; VINDER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.;
; STREET: 1100 New York Ave., N.W.
                    US-09-466-635-4
US-08-630-820-6
US-08-123-453-6
US-08-127-101A-5
US-09-027-449-72
US-09-026-985-72
US-09-027-896B-22
US-09-627-896B-22
US-09-627-896B-22
US-09-027-896-56
US-09-027-896-56
US-09-121-952A-56
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APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-NO. 6339070-1999
CLASSIFICATION - 4Uhknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 18:
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-423-439-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: D.C.
COUNTRY: U.S.A.
ZIP: 2005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 235 amino acids TYPE: amino acid
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RESULT 3
JS-09-669-971-1
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                                   PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
                                                                   140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 220;
                                                                                                                                                                                                                                                                             APPLICANT: Schwall, Ralph H.
APPLICANT: Tabor, Kelly H.
APPLICANT: Tabor, Kelly H.
TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
TITLE OF INVENTION: Atlagonists and Uses Thereof
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42; Indels
                                                                                                       LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                            LTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 751; DB 3;
Pred. No. 9.2e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/952,235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/460368
FILING DATE: 00-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Winbatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,
                                                                                                                                                                                                                              Sequence 1, Application US/08952235 Patent No. 6207152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: P09.
TELECOMMUNICATION INFORMATION:
TELEPAN: 650/952-981
TELEPAN: 650/952-981
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.3%;
71.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 220 amino acids
Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 71.84
Matches 153; Conservative
                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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                                   123
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69 TGSGSGTDFTLTITSVKADDLAVYYCQQYYAYPWTFGGGTKLBI-KRTVAAPSVFIFPPS 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 SSLIVSVGEKVTVSCKSSQSLLYISSQKNYLAWYQQKPGQSPKLLIYWASTRESGVPDRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 SGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIFPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 SALTTSPGETVTLTCRSSIGAVTTS---NYANWVQEKPDHLFTGLIGGTNNRAPGVPARF
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                                                                               APPLICANT: Schwall, Ralph H.
Tabor, Kelly H.
TITLE OF INVENTION: Hepatccyte Growth Factor Receptor
Antagonists and Uses Thereof
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/669,971 FILING DATE: 05-Jul-2001 CLASSIFICATION: Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        186 SKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/952,235
FILING DATE: <UDKNOWN>
APPLICATION NUMBER: 08/460368
FILING DATE: 02-UN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Marschang, Diane L.
REGISTRATION VINDBR: 35,600
REFERENCE/DOCKET NUMBER: P0938P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                              STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 15, Application US/09472087; Patent No. 6682736
; Sequence 1, Application US/09669971; Patent No. 6468529
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 220 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      relephone: 650/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                       NUMBER OF SEQUENCES:
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123 PPSDEQLKSGTASVVCLLMNFYPREAKVOWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
                                                                                                                                                                                25 VLTQSPSSLSVSVGDRVTMTCRAS----SSVTYIHWYQQKPGLAPKSMIYATSNLASGVP 80
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VVTOE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVOEKPDHLFTGLIGGTNNRAPGVP
                        63 ARESGSLIGDKAALTITGAQTEDEARYFCALMYSCLWVFGGGTKLTVLSRTVAAPSVFIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.2%; Score 738; DB 4; Length 235; 71.3%; Pred. No. 2e-65; tive 15; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Pillsbury Madison & Sutro, LLP
                                                                                                                                                                                                                                        183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/01975
FILING DATE: 13-AUG-1996
APPLICATION NUMBER: GB 9612295.7
FILING DATE: 12-JUN-1996
APPLICATION NUMBER: GB 9611019.2
FILING DATE: 25-MAY-1996
APPLICATION NUMBER: GB 9516810.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,769A
FILING DATE: 13-Feb-1998
CLASSIPICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.

CONDITER: 2005

COMPUTER READABLE FORM:

MEDIUM TYPE: 1.44 Mb disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HENNEGUIN, Laurent F.A.
MARSHAM, Peter R.
DOWELL, Robert I.
TITLE OF INVENTION: Chemical Compounds
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1100 New York Ave., N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                               Sequence 27, Application US/09011769A Patent No. 6436691 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 16-AUG-1995
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             Anthony M.
David C.
David H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 235 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         John F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 71.3
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLAKEY,
DAVIES,
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SLATER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HENNAM,
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US-09-011-769A-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 VVTQE-SALITSPGETVTLICRSSIGAVTISNYANWVQEKPDHLFTGLIGGTNNRAPGVP
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APPLICANT: HANSON, DOUGLAS C.
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REPERENCE: ABX.-FP.
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-112-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PARENTIN Ver. 2.1
SEQ ID NO 67
LENGTH: 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 233;
                      APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: NEVEU, MARK J.
APPLICANT: NEVEU, MARK J.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GONEWARN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PFL
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT APPLICATION NUMBER: 60/113,647
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR APPLICATION NUMBER: 60/113,647
NUMBER OF SEQ ID MOS: 147
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 65.4%; Score 740; DB 4; Length 233; Best Local Similarity 70.4%; Pred. No. 1.2e-65; Matches 152; Conservative 18; Mismatches 40; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 67, Application US/09472087
Patent No. 6682736
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-472-087-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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Best Local Simi
Matches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Ho
US-09-472-087-67
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                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 15
LENGTH: 233
TYPE: PRT
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184 TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                     179 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213
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APPLICANT: Chen, Christina Yu-Ching
TILLE REPERENCE: P1804R1
CURRENT APPLICATION WUMBER: US/10/011,125A
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/256,162
PRIOR PILING DATE: 2000-12-07
PRIOR PILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Sequence is synthesized; Patent No. 6828121
US-10-011-125A-2
                                                                                                                                                                                                    ; Sequence 2, Application US/10011125A
; Patent No. 6828121
                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 491
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                       US-10-011-125A-2
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  ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
                         SRFSGSGSGTDYTLTISSLQPEDIATYYCQHWSSKPPTFGQGTKVEV-KRTVAAAPSVFIF 139
                                                                                   PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
                                                                                                        64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIFP 123
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                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Weiner, George
APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
APPLICANT: Link, Brian
TITLE OF INVENTION: Bispecific Antibody Effective to Treat
TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 213;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,411
FILING DATE: 01-MAR-1995
CLASSIFICATION: 424
                                                                                                                                                                  LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                  LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 011823-0049
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                     US-08-397-411-12

Sequence 12, Application US/08397411

Patent No. 6129914

GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 213 amino acids
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amino acid
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Matches 152; Conservative
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STATE: California
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Sequence 79, Application US/09315926A

Factor 79, Application US/09315926A

Factor No. 6498027

GENERAL INFORMATION:

APPLICANT: Be van, Helmuth

APPLICANT: Havenga, Menzo

APPLICANT: Verlinden, Stefan

TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER

FILE REFERENCE: 2183-408008

CURRENT APPLICATION NUMBER: US/09/315,926A

CURRENT FILING DATE: 1999-05-20

FRIOR APPLICATION NUMBER: EP 99201593.3

PRIOR APPLICATION NUMBER: EP 98201693.3

PRIOR PILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 81

SEQ ID NO 79

LENGTH: 236

TENGTH: 236
                                                                                                                                                                                                                                                                                            84 RPSGSGSGTDYTLTISSLQPEDFATYYCQQYSTVPWTFGQGTKVEI-KRTVAAPSVFIFP 142
                                                                                                                                                                                                                                                                                                                                                                                                                      64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIFP 123
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                                                                                                                                                                 5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA
                                                                   .,
2
Query Match 64.9%; Score 734.5; DB 4; Length 491; Best Local Similarity 70.7%; Pred. No. 1.2e-64; Matches 152; Conservative 16; Mismatches 42; Indels 5;
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63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
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APPLICANT: HANSON, MARK J.
APPLICANT: MUELLER, EILLEN B.
APPLICANT: HANSON, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GILMAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PP1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR APPLICATION NUMBER: 60/113,647
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MUSELLE, EILLEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GILMAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PPT
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT PILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PATENTIN VET. 2.1
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200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235
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                                                                                                                                                                                                                                                                 Sequence 65, Application US/09472087
Patent No. 6682736
                                                                                                                                                                                                                                                                                                                                                               GENERAL INPORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILLAN, STEVEN C.
APPLICANT: GILLAN, GENEREY
APPLICANT: CORVALAN, JOSE R.
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Best Local Similarity
                                                                                                                                                                    RESULT 11
US-09-472-087-65
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LENGTH: 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIFPPSDEQLK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGTASVVCLLANNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:|| |:||| ||:||| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPARFSGSLI
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Sequence 14, Application US/09472087

Batent No. 6682736

GENERAL INFORMATION:

APPLICANT: HANSON, DOUGLAS C.

APPLICANT: MUELLER, EILLEN E.

APPLICANT: HANKE, JEFFREY H.

APPLICANT: GILMAN, STEVEN C.

APPLICANT: GORVALAN, JOSE R.

TITLE OF INVERTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4

FILE REFERENCE: ABX-PF1

CURRENT APPLICATION NUMBER: 60/9/472,087

CURRENT FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: 60/113,647

SOFTWARE: PATENTION TO SECOLULY OF SECOLULY
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64.7%; Score 732; DB 4; Length 235;
Best Local Similarity 69.4%; Pred. No. 7.8e-65;
Matches 150; Conservative 19; Mismatches 43; Indels
                                                                       NAME/KEY: misc feature
OTHER INFORMATION: Description of Artificial Sequence: phage
NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 64.8%; Score 734; DB 4; Length 23 Best Local Similarity 72.6%; Pred. No. 4.9e-65; Matches 151; Conservative 13; Mismatches 42; Indels
                                                                                                                                                                                                ; LOCATION: (1)..(236)
; OTHER INFORMATION: /note="hCAT1 amino acid sequence"
US-09-315-926A-79
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63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 224;
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Sequence 17, Application US/09472087

Patent NO. 6682736

GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: HANSON, BARK J.
APPLICANT: GILMAN, STEVEN E.
APPLICANT: GILMAN, STEVEN E.
APPLICANT: GILMAN, GROFFREY H.
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ASA.FFI.
CURRENT FILICATION NUMBER: US/09/472,087

CURRENT FILICA DATE: 1999-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 64.5%; Score 730.5; DB 4; Best Local Similarity 71.2%; Pred. No. 1e-64; Matches 153; Conservative 15; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGE 217
                                                                                   APPLICANT: GenPlarm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 17
LENGTH: 234
Valkirs, Gunars
Gray, Jeff
Lonberg, Nils
Biosite Diagnostics, Inc.
                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
COTHER INFORMATION: M2-32L
US-09-453-234-84
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US-09-472-087-17
                                              APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                           61 RFSGSGSGTDFTLTISSLQPEDFATYYCQQYYSTPFTFGPGTKVEI-KRTVAAPSVFIFP 119
                                                                                                                                                                                                                                                                                                                                                           124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
                                                                                                                                                                                                                                                                                                                                                                                    ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
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                                                                                                                                                                  5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA 63
                                                                                                                                                                                           3 VLTÓSPATLSLSPGERATLSCRAS---QSVSSYLAWYQQKPGQAPRLLIYDASNRAAGIP 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.5%; Score 730.5; DB 4; Length 224; 71.2%; Pred. No. 1e-64; ive 15; Mismatches 42; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 84, Application US/09456090A; Sequence 84, Application US/09456090A; Patent No. 6680209; GENERAL INFORMATION:
APPLICANT: Buechler, Joe; APPLICANT: Usuberd, Gunare, APPLICANT: Carby, Jeff; APPLICANT: Lonberg, Nils; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS; FILE REFERENCE: 0200103-00020003; CURRENT APPLICATION NUMBER: US/09/456,090A; CURRENT FILING DATE: 1999-12-06; NUMBER OF SEQ ID NOS: 110; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 84; SEQ ID NO 84;
                                                                       Length 214;
                                                                  64.5%; Score 730.5; DB 4; Length 69.8%; Pred. No. 9.7e-65; ive 20; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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Patent No. 6794132
GENERAL INFORMATION:
                                                                                           Best Local Similarity 69.89
Matches 150; Conservative
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Matches 153; Conservative
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; ORGANISM: Homo sapiens
US-09-472-087-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
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US-09-453-234-84
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7, 2005, 16:00:22 ; Search time 100 Seconds (without alignments) 785.243 Million cell updates/sec
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3: /cgn2 6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*
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15: /cgn2 6/ptodata/1/pubpaa/USOO8_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1132
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                                                                                                                                                                                                                                                                                                                                                                                                                              Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                          Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 27, Appl Sequence 28, Appl Sequence 42, Appl Sequence 1, Appli Sequence 1, Appli Sequence 4, Appli Sequence 8, Sequence 8, Sequence 4, Sequence 4, Sequence 2, Sequence 8, Description 6 US-10-625-047-27 6 US-10-625-047-28 6 US-10-723-003-42 US-09-995-693-1 0 US-09-848-832-4 4 US-10-225-108A-4 4 US-10-461-148-2 6 US-10-461-148-2 6 US-10-645-28 6 US-10-645-8 SUMMARIES 8 Query Match Length 666.22233 666.22233 666.22233 1079 1078 755.5 751 751 749.5 749.5 749.5 749.7 Score Result Š

Sequence 4, Appli Sequence 4, Appli	Sequence 122, App Sequence 122, App	Sequence 142, App	Sequence 12, Appl	Sequence 11, Appl	Sequence 15, Appl	Sequence 67, Appl	Seguence 15, Appl		Sequence 2, Appli	Sequence 587, App	Sequence 106, App	Sequence 88, Appl	Sequence 1, Appli	Sequence 10, Appl	Sequence 7, Appli	Sequence 13, Appl	Sequence 25, Appl	Sequence 5, Appli	Sequence 9, Appli	Sequence 11, Appl	Sequence 27, Appl	Sequence 38, Appl	Sequence 100, App	Ä	N	_	4	4	Sequence 52, Appl	Sequence 129, App	
US-10-704-522-4 US-10-645-215-4	US-10-307-724-122	US-10-737-290-142	US-10-435-299-12	US-10-153-382-11	US-10-612-497-15	US-10-612-497-67	US-10-776-649-15	US-10-776-649-67	US-09-807-721-2	US-10-045-674-587	US-10-128-520-106	US-10-292-088-88	US-10-364-953-1	US-10-020-786-10	US-10-764-428-7	US-10-764-428-13	US-10-764-428-25	US-10-764-428-5	US-10-764-428-9	US-10-764-428-11	US-10-764-428-27	US-10-656-769-38	US-09-056-160B-100	US-10-234-671-100	US-10-011-125-2	US-10-235-175-79	US-10-408-901-40	US-10-408-901-48	US-10-408-901-52	US-10-128-520-129	
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66.0	65.5	65.5	65.5	65.4	65.4	65.4	65.4	65.4	65.3	65.2	65.1	65.1	65.0	65.0	65.0	65.0	. 65.0	65.0	65.0	65.0	65.0	64.9	64.9	64.9	64.9	64.8	64.8	64.8	64.8	64.8	
747	742	742	741	740	740	740	740	740	739	738.5	737	736.5	735.5	735.5	735.5	735.5	735.5	735.5	735.5	735.5	735.5	735	734.5	734.5	734.5	734	733	733	733	733	
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ALIGNMENTS

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OTHER INFORMATION: Description of Artificial Sequence:native cloned OTHER INFORMATION: chimeric murine 2D12.5 light chain variable region OTHER INFORMATION: (VL) fused to human anti-tetanus toxin antibody OTHER INFORMATION: kappa light chain constant region (TTCL)
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                Sequence 277, Application US/10625047

Publication No. US20040198962A1

GENERAL INFORMATION:
APPLICANT: Meares, Claude
APPLICANT: Corneillie, Todd
APPLICANT: The Regents of the University of California
TITLE OF INVENTON: Multi-Functional Antibodies
FILE REFERENCE: 023070-130910US
CURRENT FILING DATE: 2003-07-22
PRIOR PILING DATE: 2003-07-22
PRIOR PELICATION NUMBER: US 10/350,555
PRIOR PILING DATE: 2003-07-22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
LENGTH: 218
TYPE: PRI
PRIOR FILING BATE: 2003-07-23
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
TYPE: PRIOR PILING DATE: 2003-07-23
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
TYPE: PRIOR PILING DATE: 2003-07-23
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
TYPE: PRIOR PILING DATE: 2003-07-23
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
TYPE: PRIOR PILING DATE: 2003-07-23
SOFTWARE: PatentIn Ver. 2.1
US-10-625-047-27
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SEQUENCE CHARACTERISTICS
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                         VPARFSGSLIGDKAALTIAGTQTEDEAIYFCALWYSNHWVFGGGTKLTVLSRTVAAPSVF 120
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VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence:N53C cloned OTHER INFORMATION: mutant chimeric murine 2D12.5 light chain variable OTHER INFORMATION: region (VL) fused to human anti-tetanus toxin OTHER INFORMATION: antibody kappa light chain constant region (TTCL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Publication No. US20040254108A1
GERERAL INFORMATION:
GERERAL INFORMATION:
APPLICANT: MA, Jing
APPLICANT: GHO, Yalun
TITLE OF INVENTION: PREPARATION AND APPLICATION OF
TITLE FERENCE: 549062000200
CURRENT APPLICATION NUMBER: US/10/723,003
CURRENT FILING DATE: 2003-11-26
                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Meares, Claude
APPLICANT: Meares, Claude
APPLICANT: Corneillie, Tode
TITLE OF INVENTION: Multi-Functional Antibodies
FILE REFERENCE: 023070-130910US
CURRENT FILING DATE: 2003-01-22
PRIOR APPLICATION NUMBER: US/10/625,047
CURRENT FILING DATE: 2003-01-23
PRIOR FILING DATE: 2003-01-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                    STLTLSKADYEKHKVYACEVTHQGLSLPVTKSFNRGEC 218
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Publication No. US20040198962A1
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ORGANISM: Artificial Sequence
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Best Local Similarity 95.9
Matches 209; Conservative
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LENGTH: 218
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                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      7;
                                                                                                                                                                                                                                                                                                                                                                   Query Match 66.7%; Score 755.5; DB 16; Length 235; Best Local Similarity 70.5%; Pred. No. 5.2e-56; Matches 155; Conservative 16; Mismatches 42; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Hepatocyte Growth Factor Receptor Antagonists and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 LSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/995,693
FILING DATE: 29-No. US20020136721A1-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: CN 2003101199300
PRIOR FILING DATE: 2003-11-25
PRIOR PPLICATION NUMBER: CN 031292909
PRIOR FILING DATE: 2003-06-13
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSEQ for Windows Version 4.0
ERQ ID NO 42
LENGTH: 235
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FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Synthetic Construct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09995693; Patent No. US20020136721A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Schwall, Ralph H.
Tabor, Kelly H.
                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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68

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Sequence 4, Application US/09848832
Publication No. US20030165507A1
Publication No. US20030165507A1
GENERAL INFORMATION:
APPLICANT: Hooper, Douglas
APPLICANT: Dietzschold, Bernhard
TITLE OF INVENTION: RABIES VIRUS-SPECFIC NEUTRALIZING HUMAN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND NUCLEIC ACIDS AND RELATED METHODS
FILE REFERENCE: HOOO1.NP0012
CURRENT APPLICATION NUMBER: 60/204,518
PRIOR FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 60/204,518
PRIOR PRILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                               DEQLKSGTASVVCLLANNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 185
                                                                                                                                                                                                                                                                    4 VVTQESA-LITISPGETVTLICRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
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                                                                                                                          9 SALTISPGETVTLTCRSSIGAVTTS---NYANWVQEKPDHLFTGLIGGINNRAPGVPARF
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                          Length 220;
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                                                                   42; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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; Pred. No. 1.2e-55;
14; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 749.5; DB 1
Pred. No. 1.7e-55;
                                                                                                                                                                                                                                                                                                                              SKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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Publication No. US20030157112A1
GENERAL INFORMATION:
APPLICANT: HODER, Craig
APPLICANT: DIETZSCHOLD, Bernhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.2%;
71.8%;
                                66.3%;
71.8%;
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Matches 155, Conservative
                                                                     Conservative
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                                                   Similarity
                                Query Match
Best Local Simi
Matches 153;
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US-10-232-408-1
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                                                                                                                                               Gaps
                                                                                                                                                 4
                                                                                                             Length 220;
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Publication No. US2030118587A1
GENERAL INFORMATION:
APPLICANT: Schwall, Ralph H.
Tabor, Kelly H.
TITLE OF INVENTION: Hepatcoyte Growth Factor Receptor
Antagonists and Uses Thereof
                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC comparible
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/232,408
FILING DATE: 03-Sep-2002
CLASSIFICATION: Unknown>
                                                                                                                                               42;
                                                                                                           Query Match 66.3%; Score 751; DB 9; Best Local Similarity 71.8%; Pred. No. 1.2e-55; Matches 153; Conservative 14; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                              186 SKADYEKHKVYACEVTHOGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/669,971
FILING DATE: 05-011-2001
APPLICATION NUMBER: US/08/952,235
FILING DATE: «Unknown»
APPLICATION NUMBER: 08/460368
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0938P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
; TYPE: Amino Acid
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-995-693-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Marschang, Diane L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 220 amino acids
TYPE: Amino Acid
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INFORMATION FOR SEQ ID NO: 1:
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US-10-232-408-1
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US-10-150-475A-8
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Publication No. US2004001367241

GENERAL INFORMATION:

APPLICANT: Diezschold, Bernhard

APPLICANT: Diezschold, Bernhard

APPLICANT: Diezschold, Bernhard

APPLICANT: Hooper, Douglas C.

TITLE OF INVENTYON: RECOMBINANT ANTIBODIES AND COMPOSITIONS

TITLE OF INVENTYON: RECOMBINANT ANTIBODIES AND USING THE SAME

FILE REFERENCE: 8321-110CI1-185685

CURRENT FILING DATE: 2003-06-13

PRIOR PRILING DATE: 2003-06-13

PRIOR PAPLICATION NUMBER: US 10/225,108

PRIOR PAPLICATION NUMBER: US 60/314,023

PRIOR PLING DATE: 2001-08-21

PRIOR PLING DATE: 2001-06-21

PRIOR PAPLICATION NUMBER: US 60/204,518

PRIOR PLING DATE: 2000-05-04

PRIOR PLING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 24

SOFTWARRE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: Recombinant Antibodies, and Compositions; TITLE OF INVENTION: and Methods for Making Them
FILE REFERENCE: 8321-110
CURRENT APPLICATION NUMBER: US/10/225,108A
CURRENT FILING DATE: 2003-04-10
FRIOR APPLICATION NUMBER: US 60/204,518
FRIOR APPLICATION NUMBER: US 60/204,518
FRIOR PILING DATE: 2001-05-16
FRIOR FILING DATE: 2001-05-16
FRIOR FILING DATE: 2001-06-16
FRIOR FILING DATE: 2001-08-16
FRIOR FILING DATE: 2001-08-17
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71.8%; Pred. No. 1.7e-55;
tive 13; Mismatches 43; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                               66.2%;
71.8%;
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Best Local Similarity 71.84
Matches 155; Conservative
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Best Local Similarity 71.8
Matches 155; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Human
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US-10-461-148-2
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4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP

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182
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80 ARFSGSGGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQGTKVE-FKRTVAAPSVFIF
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Sequence 8, Application US/10704522
Publication No. US20040120949A1
GENERAL INFORMATION:
APPLICANT: Adolf, Gunther
APPLICANT: Baumann, Michael
APPLICANT: Hader, Karl-Heinz
TITLE OF INVENTION: Compositions and methods for treating cancer using
TITLE OF INVENTION: cytotoxic CD44 Antibody Immunoconjugates
TITLE OF INVENTION: US/10/704,522
CURRENT APPLICATION NUMBER: US/10/704,522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTHER INFORMATION: Description of Artificial Sequence: Humanised; OTHER INFORMATION: Murine Antibody BIWA 8 Light Chain SEQ ID NO: US-10-150-475A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Adolf, G. et al.

TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
FILE REFERENCE: 1/1211
CURRENT APPLICATION NUMBER: US/10/150,475A
CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: US 60/307,451
PRIOR FILING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                 183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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63 ARFSGSLIGDKAALTITGAQTEDBARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
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                                                                      3 VLTQSPATLSLSPGERATLSCSAS----SSINYIYWYQQKPGQAPRLLIYLTSNLASGVP
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                                            123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Artificial Sequence: Humanised; OTHER INFORMATION: Murine Antibody BIWA 4 Light Chain SEQ ID NO: US-10-150-475A-4
                                                                                                                                                                                                                                                                Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41; Indels
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                                                                                                                                                     178 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213
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Publication No. US20040120949A1
GENERAL INFORMATION:
APPLICANT: Adolf, Gunther
APPLICANT: Adolf, Gunther
TITLE OF INVENTION: Compositions and methods for TITLE OF INVENTION: Compositions and methods for TITLE OF INVENTION: Compositions and methods for TITLE OF INVENTION: COMPOSITION and FILE REFERENCE: 1/1414 STOCOPY.
CURRENT PILING DATE: 2003-11-07
PRIOR APPLICATION NUMBER: US 60/429,516
PRIOR PILING DATE: 2002-11-07
PRIOR APPLICATION NUMBER: EP 02024881
PRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 9
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US-10-150-475A-4
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APPLICANT: Baum, Ankel
APPLICANT: Baum, Ankel
APPLICANT: Baum, Ankel
APPLICANT: Baum, Ankel
TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
TITLE OF INVENTION: Cyctoxic CD44 Antibody Immunoconjugates and
TITLE OF INVENTION: Cyctoxic CD44 Antibody Immunoconjugates and
TITLE OF INVENTION: Chemotherapeutic Agents
FILE REFERENCE: 1/1383
CURRENT FILING DATE: 2003-08-21
PRIOR APPLICATION NUMBER: EP 02 018 686.2
PRIOR APPLICATION NUMBER: US 60/405,956
PRIOR PILING DATE: August 21, 2002
PRIOR FILING DATE: August 26, 2002
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                         OTHER INFORMATION: Humanised Murine Antibody BIWA 8 Light Chain
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                                                                                                                                                                                                                                                                                                 Query Match 66.2%; Score 749; DB 16; Length 213; Best Local Similarity 72.2%; Pred. No. 1.7e-55; Matches 156; Conservative 14; Mismatches 40; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/429,516
PRIOR FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: EP 02024881
PRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 9
SOFWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 213
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Publication No. US20040126379A1
GENERAL INFORMATION:
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SEQ ID NO 8
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; Sequence 4, Application US/10645215
; Publication No. US20040126379A1
; GENERAL INFORMATION:
    APPLICANT: Adolf, Guenther
    APPLICANT: Adolf, Guenther
    APPLICANT: Heider, Karl-Heinz
    TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
    TITLE OF INVENTION: Chemotherapeutic Agents
    TITLE OF INVENTION: UNBER: US 00.045,215
    CURRENT APPLICATION NUMBER: US 00.045,956
    PRIOR FILING DATE: August 26, 2002
    NUMBER OF SEQ ID NOS: 9
    SOFTWARE: PatentIn Ver. 2.1
    SEQ ID NO 4
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66.0%; Score 747; DB 16; Length 213;
Best Local Similarity 72.2%; Pred. No. 2.4e-55;
Matches 156; Conservative 13; Mismatches 41; Indels
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                                                                                                                  TYPE: PRT ORGANISM: Artificial Sequence
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SOFTWARE: Patentin Ver. 2.1
                              SEQ ID NO 4
LENGTH: 213
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APPLICANT: Bowdish, Katherine S.
APPLICANT: Bowdishaw, Mark
TITLE OF INVENTION: RATIONALLY DESIGNED ANTIBODIES
FILE REFERENCE: 1087-2cip
CURRENT APPLICATION NUMBER: US/10/307,724
CURRENT PAPLICATION NUMBER: US 60/251,448
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR APPLICATION NUMBER: US 60/251,448
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR APPLICATION NUMBER: US 60/294,068
PRIOR PILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-29
PRIOR FILING DATE: 2001-10-5
PRIOR FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 134
SOFTWARE: PATENT NOS: 134
SOFTWARE: PATENT NOS: 134
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                        178 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 65.5%; Score 742; DB 15; Best Local Similarity 70.8%; Pred. No. 6.6e-55; Matches 153; Conservative 16; Mismatches 43;
183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: antibody light chain US-10-307-724-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7, 2005, 16:18:38
                                                                                                                                                                            ; Sequence 122, Application US/10307724; Publication No. US20030232972A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: June
                                                                                                                                                         US-10-307-724-122
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- protein search, using sw model OM protein

June Run on:

7, 2005, 15:39:10 ; Search time 25 Seconds (without alignments) 839.010 Million cell updates/sec

US-09-671-953B-5 1132 1 RSAVVTQESALTTSPGETVT......BVTHQGLSXPVTKSFNRGEC 218 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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,	* Query	Match	65.4	64.4	64.0	63.3	60.3	59.6	51.1	48.8	48.1	48.0	47.4	46.9	46.7	46.1	46.0	45.9	45.7	45.5	45.4	45.0	45.0	45.0	44.7	44.5	44.4	44.3	44.1	44.0	,
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495.5	492	492	488.5	485	484.5	482	482	482	477	477	475.5	472	469
30	32	ე წ ე 4	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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JEG0242

JEG0242

JEG0242

G Rappa chain NIG26 precursor - human

C;Species: Homo sapiens (man)

C;Accession: JEG0242

R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, submitted to JIPID, November 1998

A;Description: Structure relationship of kappatype light chains with AL amyloidosis: Mu A;Reference number: JEG0241

A;Reference number: JEG0241

A;Reference number: JEG0241

A;Reference structure relationship of kappatype light chains with AL amyloidosis: Mu A;Reference number: JEG0241

A;Reference number: JEG0242

A;Reference structure relationship of kappatype light chains with AL amyloidosis: Mu A;Reference number: JEG0241

A;Referenc
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Query Match
65.4%; Score 740; DB 2; Length 215;
Best Local Similarity 70.4%; Pred. No. 7.9e-49;
Matches 152; Conservative 17; Mismatches 43; Indels

ä; 4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62 **Gaps** 4, à

63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122 g ò

PPSDEQLKSGTASVVCLLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182 셤 ઠ

183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218 d à

180 셤

JE0244

JE0244

JE0244

JEO244

JEO244

JEO244

JEO245

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181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Bate: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 21-Jan-2000
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 21-Jan-2000
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 21-Jan-2000
R;Kwak, J.W.; Choi, B.K.; Lee, D.I.; Kang, Y.K.; Seo, Y.G.; Cho, W.K.; Han, M.H.
Gene 169, 237-239, 1996
A;Title: Cloning and characterization of cDNAs coding for heavy and light chains A;Reference number: PC4155; MUID:96194809; PMID:8647454
A;Residues: 1-244 < kWAA
A;Residues: 1-244 < kWAA
A;Cross-references: GB:U28967; NID:g1262179; PIDN:AAC52488.1; PID:g1262179
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-214/Product: light chain #status predicted <MAT>
F;2-214/Residuer: V region.
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C;Species: Mus musculus (house mouse)
C;Date: 10-May_1996 #sequence_revision 19-Jul-1996 #text_change 21-Jan-2000
                                                                                                                                                               ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLW---VFGGGTKLTVLSRTVAAPSV
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                                                                                                                       VLTOSPATLSVSPGERATLSCRAS -- OSVHSNLA - WYQOKPGQAPRLLIYRASTRATGIP
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Query Match 64.4%; Score 729; DB 2; Best Local Similarity 71.2%; Pred. No. 5.4e-48; Matches 156; Conservative 14; Mismatches 39
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66.5%; Pred. No. 1.2e-47;
iive 23; Mismatches 43
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Matches 145; Conservative
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Ig kappa chain Am37 precursor - human Cispecies: Homo spains (man) Cispecies: Homo spains (man) Cispecies: Homo spains (man) Cispecies: Homo spains (man) Cispecies: Os-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000 Ciscession: JE0241 Cispecies: JE0241 Januaki, S.; Hossani, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T submitted to JIPID, November 1998 A; Description: Structure relationship of kappatype light chains with AL amyloidosis: Mul
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                                                             immunoglobulin homology
<IMM>
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                                                                                                                                                                  63.3%; Score 716; DB 2; 69.7%; Pred. No. 5.1e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 60.3%; Score 682.5; DB 2
Best Local Similarity 66.8%; Pred. No. 1.7e-44;
Matches 145; Conservative 14; Mismatches 53.
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                                                                                                                                                                                                                               13; Mismatches
A;Molecule type:.protein
A;Residues: 1-215 cALI-
C;Superfamily: immunoglobulin V region;
F;16-90/Domain: immunoglobulin homology
                                                                                                                                                                                                    Best Local Similarity 69.7*
Matches 152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: JE0241
A;Accession: JE0241
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                                                                                                                                                                                                 Similarity
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A, Reference number: A94417
A, Contents: Bence Jones protein Roy
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A; Residues: 1-106 <HIE>
                                                                                                                                                                                                   Best Local Similarity
Matches 117; Conser
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C;Crowe, J.S.; Smith, M.A.; Cooper, H.J.

Nucleic Anders Res. 17, 7992, 1989

A;Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA

A;Reference number: S06084; MUID:90016888; PMID:2508067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiems (man)
C;Species: Homo sapiems (man)
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 08-Sep-2000
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 08-Sep-2000
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 08-Sep-2000
R;Parances, V.; Pandrau-Garcia, D.; Guret, C.; Ho, S.; Wang, Z.; Duvert, V.; Saeland, S. EMBO J. 13, 5937-5943, 1994
A;Frances, V.; Pandrau-Garcia, D.; Guret, C.; Ho, S.; Wang, Z.; Duvert, V.; Saeland, S. EMBO J. 13, 5937-5943, 1994
A;Reference number: S52059; MUID:95112804; PMID:7813432
A;Status: preliminary
A;Residues: Preliminary
A;Residues: 1-135 < FRA>
C;Superfamily: pre-B cell omega light chain; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                     63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
                                                                                                                                                                                                                                                                                                                                                                    61 DRFSGSGSGTDFTLTISRLEPEDFAVYYGQQYGSSPLTFGGGTKVEI-KRTVAAPSVFIF 119
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C;Date: 28-Peb-1990 #sequence_revision 28-Peb-1990 #text_change 21-Jan-2000
C;Accession: S06084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
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                                                                                                                                                               Length 215;
A;Accession: A23746
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-215 < LEGO-
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;16-91/Domain: immunoglobulin homology < IMM>
                                                                                                                                                            Query Match 59.6%; Score 675; DB 2; Length 21 Best Local Similarity 68.8%; Pred. No. 6.3e-44; Matches 148; Conservative 15; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.1%; Score 578.5; DB 2 89.7%; Pred. No. 7.2e-37; ive 3; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig kappa chain precursor - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 89.7
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FNRGEC 218
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FNRGEC 135
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A;Accession: A91651
A;Molecule type: protein
A;Residues: 1-106 <SUT>
R;Hieter, P.A.; Max, E.E.; Seidman, J.G.; Maizel Jr., J.V.; Leder, P.
R;Hieter, P.A.; Max, E.E.; Seidman, J.G.; Maizel Jr., J.V.; Leder, P.
A;Hieter, P.A.; Max, E.E.; Seidman, J.G.; Maizel Jr., J.V.; Leder, P.
A;Hieter, Cloned human and mouse kappa immunoglobulin constant and J region genes conser
A;Reference number: A90806; MUID:81042304; PMID:6775818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:J00241; NID:g33140; PIDN:CAA23823.1; PID:g1335148
A;Note: the sequence was determined from the germline gene
R;Hilschmann, N.; Barnikol, H.U.; Hess, M.; Langer, B.; Ponstingl, H.; Steinmetz-Kayne, in Gamma Globulins: Structure and Function, Franck, F.; and Shugar, D., eds., pp.57-74,
                                                                                                                                                                                                                                                                                                                                                                                                                 119
                                                                                                                                                                                                                                                                                                                                                                                                                                             FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 SIFPPSTEQLATGGASVVCLMNNFYPRDISVKWKIDGTERRDGVLDSVTDQDSKDSTYSM 201
                                                                                                                                                                                                                                                                                                                                                               82
                                                                                                                                                                                                                                                                                                                                          GVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSV
                                                                                                                                                                                                                                                                                                                 VVTQE-SALITSPGETVTLICRSS---IGAVTISNYANWVQEKPDHLFIGLIGGINNRAP
A;Molecule type: mRNA
A;Residues: 1-240 <CRO-
A;Cross-references: EMEL:X16129; NID:956457; PIDN:CAA34256.1; PID:956458
A;Cross-references: EMEL:X16129; NID:956457; PIDN:CAA34256.1; PID:956458
C;Superfamily: immunoglobulin V region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
F;21-240/Promain: ignal sequence #status predicted <SIG>
F;21-240/Product: Ig kappa chain #status predicted <MAT>
F;153-222/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                      S.
                                                                                                                                                                                                                   Length 240;
                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                      73;
                                                                                                                                                                                                                48.8%; Score 552.5; DB 2
llarity 53.4%; Pred. No. 1.2e-34;
Conservative 24; Mismatches 73
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Query Match
Best Local Similarity 96.3%;
Matches 104; Conservative
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                     Biochem. 122, 322-329, 1997
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A;Molecule type: DNA
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A, Molecule type: protein

A, Residnes: 144, A, A, 46-56, O, 750-52, 17, 84-106 cHIL)

A, Residnes: Tat's sequence has the Inv (1.2) allocypic marker, 45-Ala and 831-Euu

A, Horse chis sequence has the Inv (1.2) allocypic marker, 45-Ala and 831-Euu

A, Accession: A, 2016 cHID.

A, A, A, Contents: Bence Jones protein Cum

A, A, Contents: Bence Jones protein Cum

A, Title: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete

A, Title: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete

A, Title: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete

A, Title: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete

A, Accession: A, 2017, MID: 5024134; PMID: 4893682

A, Contents: Bence Jones protein. Ag

A, Title: Marker Contents: Bence Jones protein. Ag

A, Title: Marker Contents: A, 2017, MID: 70214734; PMID: 4893682

A, Accession: A, 2017, MID: 2017, PMID: 201
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pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein C;Species: synthetic
C;Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 06-Nov-1998
C;Accession: PC4402
R;Suzuki, C.; Ueda, H.; Suzuki, E.; Nagamune, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.1%; Score 544; DB 1; Length 10 llarity 99.1%; Pred. No. 2.2e-34; Conservative 0; Mismatches 1; Indels.
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Matches
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A,Title: Construction, bacterial expression, and characterization of hapten-specific sin A,Reference number: PC4402
A,Accession: PC4402
A,Accession: PC4402
A,Molecule type: DNA
A,Residues: 1-287 <802>
C,Keywords: fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C,Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000 C,Accession: A31790 #Sequence_revision 31-Mar-1990 #text_change 11-Jan-2000 C,Accession: A31790 #Sequence, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A. J. Biol. Chem. 263, 17100-17105, 1988 A;Fitle: Preliminary crystallographic data, primary sequence, and binding data for an an A;Reference number: A92686; WUID:89034213; PMID:3182835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SVFIFPPSDEQLKSG-TASVVCLLNNFYPREAKVQW----- 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mus musculus (house mouse)
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 AVVTQESALITSPGETVILICRSSTGAVITSNYANWVQEKPDHLFTGLIGGINNRAPGVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --KVDNALQSG-----NSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAC 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:X82687; NID:g673448; PIDN:CAA58008.1; PID:g673449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Berdoz, J.; Kraehenbuhl, J.P.
submitted to the EMBL Data Library, November 1994
A;Description: Specific amplification by the polymerase chain reaction of
A;Reference number: S52445
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                   47;
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                                                                                                                                                                                                                                      Length 287;
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-111/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                   49;
                                                                                                                                                                                                                                      DB 4;
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Pred. No. 9.1e-34;
0; Mismatches 4.
                                                                                                                                                                                                                                   Query Match
48.0%; Score 543.5; DB 4
Best Local Similarity 53.4%; Pred. No. 6.9e-34;
Matches 126; Conservative 14; Mismatches 49
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C,Complex: 10,4 immunoglobulin heterotetramer subunit consists of two identical light (ka, hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l. (;Superfamily: immunoglobulin V region; immunoglobulin homology (;Keywords: heterotetramer; pyroglutamic acid (;Keywords: heterotetramer; pyroglutamic acid (;L19)Domain: signal sequence #status experimental <SIG>P;20-129)Domain: Ig lambda-1 chain precursor V region #status experimental <MAT>P;20 hodified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimer P;41-109/bisulfide bonds: #status predicted
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                                                                                                                                                                    A; Contents: H2020
A; Accession: A90780
A; Molecule type: DNA
A; Residues: 1-43, T', 45-50,'G',52-58,'E',60-89,'D',91-129 <BER>
A; Note: the sequence was determined from the differentiated gene
A; Note: the sequence was determined from the differentiated gene
A; Note: 198, 380-382, 1982
A; Title: Somatic variants of murine immunoglobulin lambda light chains.
A; Reference number: A93282; MUD: 82220143; PMID: 6283385
R;Bernard, O.; Hozumi, N.; Tonegawa, S.
Cell 15, 1133-1144, 1978
A;Title: Sequences of mouse immunoglobulin light chain genes before and after somatic
A;Reference number: A90780; MUID:79084170; PMID:103630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 AVVIQESALITSPGETVILICRSSIGAVITSNYANWVQEKPDHLFIGLIGGINNRAPGVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 AVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQOKPDHLFTGLIGGTNNRAPGVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: DNA
A,Residues: 1-58, E',60-89,'D',91-98,'T',100-105,'M',107-129 <BOJ
A,Note: the sequence was determined from the differentiated gene
C,Comment: The MOPC 104E sequence is shown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 129;
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50.5%; Pred. No. 2.3e-32;
iive 29; Mismatches 72
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Pred. No. 3.7e-33;
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Best Local Similarity 94.4%;
Matches 102; Conservative
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Best Local Similarity 50.5
Matches 109; Conservative
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A;Residues: 1-235 <FIS>
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A;Accession: C93282
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C;Species: Mus musculus (house mouse)
C;Date: 24-Sep-1981 #sequence revision 24-Sep-1981 #text change 09-Jul-2004
C;Date: 24-Sep-1981 #sequence revision 24-Sep-1981 #text change 09-Jul-2004
C;Date: 24-Sep-1981 #sequence revision 24-Sep-1981 #text change 09-Jul-2004
R;Burstein: Y; Schechter; I.
Proc. Natl. Acad. Sci. U.S.A. 74, 716-720, 1977
A;Title: Amino acid sequence of the NH-2-terminal extra piece segments of the precursors A;Reference number: A93815; MUID:77148916; PMID:403522
A;Contents: MOPC 104B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 show no differences from MOPC 104B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig lambda-1 chain precursor V regions (MOPC 104E, RPC20, J558, S104, S178, H2020, S43)
                                                             A;Molecule type: mRNA
A;Residues: 1-220 <SCH>
A;Cross-references: GB:MJ3626; GB:J04061; NID:g533234; PIDN:AAA39162.1; PID:g533235
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Reywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 20-43,'N',45-70,'N',72-115,'R',117-129 <CE3> A;Note: these proteins were isolated from serum or urine of tumor-bearing
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 68, 590-594, 1971
A;Title: Amino acid sequences of two mouse immunoglobulin lambda chains.
A;Reference number: A93775; WUID:71107854; PMID:5276767
A;Contents: MOPC 104E; RPC 20
                                                                                                                                                                                                                                                                                                                                                                                                                           5.
                                                                                                                                                                                                                                                                                                                                        Length 220;
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Cesari, I.M.; Weigert, M.
Proc. Natl. Acad. Sci. U.S.A. 70, 2112-2116, 1973
A;Title: Mouse lambda-chain sequences.
A;Teference number: A93784; MUID:73229669; PMID:4516208
A;Contents: J558; S104; S178
                                                                                                                                                                                                                                                                                                                                    Query Match 46.9%; Score 530.5; DB 2; Best Local Similarity 51.6%; Pred. No. 5e-33; Matches 113; Conservative 26; Mismatches 75;
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A,Residues: 20-129 <AP2>
A,Note: compositions and partial sequences of RPC
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A,Residues: 'Z', 21-25,'Q',27-129 <APP>
A,Accession: C93775
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A, Molecule type: protein
A, Residues: 1-29 < BUR>
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A, Residues: 20-129 <CES>
A, Accession: B93784
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A;Residues: 20-43,'N',45-
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RESULT 15
S06819
IG lambda chain V region (clone 10C3) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 11-Nov-1994 #text_change 21-Jan-2000
C;Accession: S06819
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Titler iComparative sequence and immunochemical analyses of murine monoclonal anti-morp
A;Reference number: S06819
A;Accession: S06819
A;Accession: S06819
A;Accession: S06819
A;Accession: S06819
A;Cross-references: EMBL:X17168; NID:g52251; PIDN:CAA35046.1; PID:g930172
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;14-91/Domain: immunoglobulin homology 
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123 PPSDEQLKSGTASVVCLLANNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
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46.0%; Score 521; DB 2; Length 11:
Best Local Similarity 94.4%; Pred. No. 1.3e-32;
Matches 102; Conservative 1; Mismatches 5; Indels
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                                                   7, 2005, 15:37:31 ; Search time 111 Seconds (without alignments) 1005.705 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                      hits satisfying chosen parameters:
                                                                                                                                                  1612378 seqs, 512079187 residues
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LV1E MOUSE
LV1D MOUSE
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Q8CGS1
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum Match 1008
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Maximum DB seq length: 200000000
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ALIGNMENTS
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Strausberg R.;
Submitted (CCT-2001) to the
EMBL, BC016380; AAH16380.1;
HSSP; P01837; IKCU.
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                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                     Hypothetical protein.
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Q6PJF2;
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Q6PJF2
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                          Length 235;
                                                                                              42; Indels
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL. BC073792. AAH73792.1; -.
InterPro; IPR0013599; Ig.
InterPro; IPR00110; Ig-like.
InterPro; IPR00110; Ig-like.
InterPro; IPR001597; Ig-c1.
InterPro; IPR001596; Ig-MHC.
Pfam; PPF054; C1-set; I.
Pfam; PPF00647; Ig; 2.
Hypothetical protein.
SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                       64.8%; Score 734; DB 2; 70.4%; Pred. No. 1.5e-56;
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                                                                          Best Local Similarity 70.4%; Pred. No. 1.5e
Matches 152; Conservative 18; Mismatches
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Altausherg R. L., Feingold E. A., Grouse L. H., Derge J. G.,
Altausherg R. D., Collins F. S., Wagner L., Shenmen C. M., Schuler G. D.,
Altschul S. P., Zeeberg B., Buetow K. H., Schaefer C. F., Bhat N. K.,
Altschul R. F., Jordan H., Moore T., Max S. I., Wang J., Haich F.,
Battleron M., Soares M. B., Bonaldo M. F., Casavant T. L., Scheetz T. E.,
Brownstein M. J., Usdin T. B., Tochiyuki S., Carninci P., Prange C.,
Raha S. S., Loquellano N. A., Peters G. J., Abramson R. D., Mullahy S. J.,
Boaks S. A., McKernan R. J., Malek J. A., Gunarathe P. H.,
An Islandon D. K., Muzny D. M., Sodergren E. J., Lu X., Gibbs R. A.,
Anting M., Madan A., Young A. C., Shevchenko Y., Bouffard G. G.,
Mhiting M., Madan A., Young A. C., Shevchenko Y., Bouffard G. G.,
Anting M. Madan A., Young A. C., Shevchenko Y., Bouffard G. G.,
Anting M. J., Skalska U., Schmutz J., Myers R.M., Butterfield Y. S.,
Androes S. J., Marra M. J.,
Jones S. J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                       Length 235;
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073191; AAH73791.1; -.
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
SWART; SM00409; IG; 2.
SWART; SM00407; IGG-1; 1.
PROSITE; PS00815; IG_LIKE; 2.
PROSITE; PS00280; IG_MHC; UNKNOWN_1.
PHYDCHELICAL DYCLEIN.
SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                             Query Match

64.8%; Score 733; DB 2;
Best Local Similarity 70.5%; Pred. No. 1.9e-56;
Matches 153; Conservative 17; Mismatches 41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199 TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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05-JUL-2004 (TrEMBLrel. 27, Le
05-JUL-2004 (TrEMBLrel. 27, Le
Hypothetical protein.
Homo sapiens (Human).
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TISSUE=Spleen;
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124
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DR DR DR BER
SO DR SE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 RCAIQMTQSPSSLSASVGDRVTITCRASQG---ISNDLGWYQQKPGKAPKLLIYAASSLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59 PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 236;
InterPro; IPR003597; Ig_cl.
InterPro; IPR003065; Ig_MHC.
InterPro; IPR003396; Ig_v.
Pfam; P070545; Cl.set; 1.
Pfam; P707654; Cl.set; 1.
SMART; SM00409; IG; 2.
SMART; SM00406; IGv. 1.
SMART; SM00406;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64.7%; Score 732; DB 2; 70.0%; Pred. No. 2.3e-56;
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TISSUE=Skeletal Muscle;
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TISSUE=Skeletal Muscle;
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Best Local Similarity
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Q7Z3Y4
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RA MEDLINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA MEDLINE=2338257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Altechul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
Diacchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Workerran K.J., Malek J.A., Gunarane P.H.,
RA Brownstein M.S., Morker K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodercia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Morley K.C., Shevchenko Y., Bouffard G.G.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Ra Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Ry Jones S.J., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 RFSGSLIGDKAALTITGAQTEDEARYFCALMYSCLWVFGGGTKLTVLSRTVAAPSVFIFP
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 236;
                        to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;
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Last annotation update)
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70.7%; Pred. No. 5.7e-56;
ive 15; Mismatches 43
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                                                                                                                      INCEPPO: JPR007110; IG-like.
INCEPPO: JPR003597; IG_C1.
INCEPPO: JPR003597; IG_MHC.
INCEPPO: JPR003596; IG_MHC.
PEam; PF07654; C1-8et; I.
PR0051TE; PS00406; IGV: L.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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Strausberg R.;
Submitted (WAR-2001) to the
EMBL; BCOG5332.1;
HSSP; P01834; 1HEZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 152; Conservative
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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SEQUENCE FROM N.A.
                                                        SEQUENCE FROM N.A
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                                                                                        rissue=Lung;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 VPIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RSAV-VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRA 58
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Hypothetical protein.
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                         Strausberger R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL BGOSS26, AAH56256.1;
HSSP, P01834; HHZ.
InterPro; IPR001359; Ig_cl.
R InterPro; IPR001359; Ig_cl.
R InterPro; IPR001506; Ig_MHC.
R InterPro; IPR001506; Ig_WHC.
R InterPro; IPR001506; Ig_WHC.
R Pfam; PR07654; Cl.set; 1.
R SMART; SM00406; IGV; 1.
R PROSITE; PS50835; IG_LIKE; 2.
R PROSITE; PS50836; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                            234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.2%; Score 727; DB 2;
68.2%; Pred. No. 6.3e-56;
iive 20; Mismatches 44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 68.2
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein SEQUENCE 234 AA;
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SEQUENCE FROM N.A.
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05-JUL-2004
05-JUL-2004
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TISSUB—Primary B-Cells;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

K Straueberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

A patchench L., Marusina K.R., Farmer A.A., Rubin G.M., Hong L.,

B tapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

B Robas S.A., McGEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bulfard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIFP 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 PSDEQLKSGTASVVCLLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 LTQSPSFLSASVGDRVTITCRASQG----ISSYLAWYQQKPGKAPNLLIYAASTLQSGVPS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 RFSGSGSGTEFTLTISSLQPEDFATYYCQQLNSSPPTFGGGTKVEI-KRTVAAPSVFIFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 236;
Strausberg<sup>R.,</sup>
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC034141; AAH34141.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 236 AA; 25603 WW, 8BC561106861213F CRC64;
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27, Last sequence update)
27, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
63.9%; Score 723.5; DB 2
Best Local Similarity 70.7%; Pred. No. 1.3e-55;
Matches 152; Conservative 14; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 AA.
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                                                                                                                                InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
InterPro; IPR003596; Ig_V.
Efam; PR07654; Cl-set; I.
SMART; SM004007; IGc1; I.
SMART; SM004007; IGC1; I.
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Local Similarity
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MEDLINE-22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;
Straubsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaffer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Uggin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 VTQE-SALTISPGETVILICRSSIGAVITSNYANWVQEKPDHLFTGLIGGINNRAPGVPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 236;
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                                                                                                                                                     Strausberg R.;
Strausberg R.;
Submitted (UND-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO73/763; AAH73763.1; -.
InterPro; IPR0013599; Ig. InterPro; IPR0013597; Ig. InterPro; IPR0013597; Ig. InterPro; IPR0013597; Ig. InterPro; IPR0013596; Ig. MHC.
InterPro; IPR0013596; Ig. WHC.
Pfam; PP07643; Cl-8et; I.
                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEGUENCE 236 AA; 25924 MW; FDE2093DC560CFF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06P5S8;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.8%; Score 722.5; DB 2;
69.3%; Pred. No. 1.6e-55;
iive 18; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     236
                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149; Conservative
                                                                                                                                                                                                                                                                                                                        SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 1.
SMART; SM00406; IGv; 1.
                                                                         вефпенсев.
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                                                                                                                     SEQUENCE FROM N.A.
TISSUE-Primary B-Cells;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
                                                                         CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Hellron E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Rzzywinski M.I., Skalska U., Smailus D.E., Schmerch A., Schein J.E., Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 ARFSGSLIGDKAALTITGAQTEDEARYFCALW-YSCLWVFGGGTKLTVLSRTVAAPSVPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 VLTQSPGTLSFSPGERATLSCRAS--QTVFSSHLAWYQQRPGQAPRLLIYGASSRATGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
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TISSUSESPLEADER:
TISSUSESPLEADER:
TISSUSESPLEADER:
SUBSUSESPLEADER:
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Allschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A HARSY; PURSJ; 1ACO.

A INTERPRO; IPR0031309; IG.

A INTERPRO; IPR003110; IG-like.

A INTERPRO; IPR003006; IG_MHC.

A INTERPRO; IPR003006; IG_MHC.

A INTERPRO; IPR003006; IG_WHC.

A SMART; SM00409; IG.; 2.

B SMART; SM00406; IGV; 1.

A SMART; SM00406; IGV; 1.

B ROSITE; PS00290; IG_MHC; UNKNOWN_1.

A HYPOCHECICAL DYOCCELIN.

A HYPOCHECICAL DYOCCELIN.

B ROSITE; PS00290; IG_MHC; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Straugherg R.; Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases EMBL; BC062704; AAH62704.1; -. HSSP; P01837; IKCU.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218
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                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 TLTLSKADYEKHKVYACEVTHOGLSXPVTKSFNRGEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Glandular pool- thyroid;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 152; Conservative
                                                                                                                                                                                                                                                                                  cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.W., Sodergren B.M., Gay L.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A. Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butcerfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
The Mark M. J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLTQSPGTLSLSPGERAALSCRAS--QSVNSKYLAWYQQKPGQAPRLLMYAASIRATGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Hymo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47; Indels
                                                                                                                                                                                                                                                               Strausberg R.,
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases
EMBL; BC073793; AAH73793.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l protein.
235 AA; 25646 MW; DF32B580BAD19E4B CRC64;
                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.7%; Score 721; DB 2;
69.4%; Pred. No. 2.1e-55;
ive 15; Mismatches 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                    InterPro; IPR003599; Ig.
InterPro; IPR003110; Ig-11ke.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_V.
Pfam; PP00407; Ig_V.
Pfam; PP00407; Ig_V.
SMART; SM00409; IG; 2.
SMART; SM00409; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 69.43
Matches 150; Conservative
                                                                                                                                                                                            and mouse cDNA sequences.
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                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                  TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical
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SEQUENCE FROM N.A. NCBI_TaxID=9606;

TISSUE=Spleen;

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RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Rtausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rapleton M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Rapleston M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Robask S.A., McEwan P.J., McKernan K.J., Malek J.B., Mullahy S.J.,

Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Radiques S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Radriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Nilalon D.K., Marra M.A.,

Jones S.J., Marra M.A.,

Jones S.J., Marra M.A.,

Jones S.J., Marra M.A.,

""" "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVFIFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
R EMBL, BC073775; AAH73775.1; -.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR003599; Ig.
R InterPro; IPR003597; Ig.
R InterPro; IPR003596; Ig.
R InterPro; IPR003596; Ig.
R InterPro; IPR003596; Ig.
R Ffam; PF07654; C1-set; I.
R Pfam; PF07654; C1-set; I.
R Pfam; PR00409; Ig; 2.
R SMART; SM00409; IGC1; 1.
R SMART; SM00406; IGC1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypotheitcal protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 63.6%; Score 720.5; DB 2 Best Local Similarity 69.3%; Pred. No. 2.4e-55; Matches 149; Conservative 17; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Spleen;
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1D Q6
AC Q6
DT 05
DT 05
DT 05
OS H0
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                   Astraubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.P., Zeeberg B., Buetow K.H., Schafer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWV-FGGGTKLTVLSRTVAAPSVFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                       TISSUE=Brain;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR0013599; Ig.
InterPro; IPR00110; Ig-like.
InterPro; IPR003599; Ig.
InterPro; IPR003306; Ig_MC.
InterPro; IPR003596; Ig_V.
Pfam; PF07654; Cl.set; I.
SMART; SM00409; IG; 2.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_I.
PROSITE; PS00290; IG_MHC; UNKNOWN_I.
Hypothetical protein.
SEQUENCE 236 AA; 25834 MW; 6647A9E77A3C0053 CRC64;
       Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.4%; Score 717.5; DB 2 69.6%; Pred. No. 4.4e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; BC032451; AAH32451.1;
HSSP; P01837; 1KCU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Brain;
                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Simi
Matches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
          OCC REAL STREET 
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TISSUE=Primary B-Cells;

RX TISSUE=Primary B-Cells;

REDINE=22388557; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchehot L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Rohards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Mriting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Rayainski M.I., Skatska U., Smailus D.E., Schnerch A., Schein J.E.,

R Morayainski M.I., Skatska U., Smailus D.E., Schnerch A., Schein J.E.,

R Andrayanski M.A.;

R and Mause C.DN sequences "."

R and mouse C.DN sequences "."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTQE-SALTISPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 MTQSPSSVSASVGDRVTITCRASQG---ISSWLAWYQQKPGKAPKILIYAASSLQSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073764; AAH73764.1; -.
InterPro; IPR003599; Ig. 11ke.
InterPro; IPR00710; Ig-11ke.
InterPro; IPR003597; Ig. cl.
InterPro; IPR00306; Ig_WHC.
InterPro; IPR00306; Ig_W.
InterPro; IPR00306; Ig_W.
InterPro; IPR00306; Ig_W.
InterPro; IPR00309; Ig. 2.
InterPro; IPR00309; Ig. 2.
INTERPRO; IGC; 1.
INTERPRO; IGC; 2.
INTERPRO; IGC; 3.
INTERPRO; IGC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 63.2%; Score 715.5; DB 2
Best Local Similarity 69.3%; Pred. No. 6.6e-55;
Matches 149; Conservative 19; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                  [1]
SEOUENCE FROM N.A.
                                                                                                                                             NCBI_TaxID=9606;
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236 AA

05-JUL-2004 (TrEMBLrel. 27, Created)

PRELIMINARY;

Q6GMX8

RESULT 12 Q6GMX8

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MEDINE-2288257; PubMed=12477912; DOI=10.1073/pnas.242601899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wubin G.M., Heiber R.D.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wubin G.M., Heiber R.D.,
Altschul M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.F.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.F.,
A.M. McZwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Bosak S.A., McZwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A.Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A.Hilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A.Hiting M., Madan A., Young A.C., Shevchento Y., Bouffaud G.G.,
A.Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A. Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A. Marra M.A.,
A. Jones S.J., Marra M.J., Marra M.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKYDNALQSGNSQESVTEQDSKDSTYS 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 RCAIQLTQSPSSLSASVGERVTITCRASQG---ISSALAWYQQKPGKPPKLLIYDASTME 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RSAV-VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGVPSRFSGSGSGTHFTLTISSLQPEDFATFYCQQFKSYPRTFGQGTTLEI-KRTVAAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Gaps
                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.2%; Score 704; DB 2; Length 23(69.1%; Pred. No. 6.8e-54; ive 15; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: BCO29444; AAH29444.1; -.
HSSP; P01607; 1AR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS0299; IG_MHC; UNKNOWN_1.
Hypotherical protein.
SEQUENCE 236 AA; 25741 MW; BD50AF071FEEE351 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                          Last sequence update)
Last annotation update)
                                      236 AA
                                                                           Created)
                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003599; IG.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003596; Ig.MC.
InterPro; IPR003596; Ig.WHC.
InterPro; IPR003596; Ig.V.
Pfam; PF07654; Cl-set; I.
SMART; SM00407; IGc1; I.
SMART; SM00407; IGc1; I.
                                                                       05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
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                                    PRELIMINARY;
                                                                                                                           Hypothetical protein.
Homo sapiens (Human).
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                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                  NCBI_TaxID=9606;
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Straubberg R.L., Feingold E.A., Grouse J.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L.H., Derge J.G., Straubberg R.L., Feingold E.A., Grouse L.H., Borge J.G., Straubberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschuls R.F., Jordan H., Moore T., Max S.T., Wang J., Hashe F., Stapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McZwan P.J., McKernan K.J., Malke J.A., Gunzarne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Halton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Shevchenko Y., Butterfield Y.S., Schiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Jones S.J., Marra M.A., Smailus D.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schner A., Schein J.E., Schner Han IS,000 full-length human and manalysis of more than 15,000 full-length human and some sunday and sunday and some sunday sunday and some sunday and some sunday and some sunday and some 
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO34146; AAH34146.1; -.
HSSP; PO1607; 1AR2.
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SEQUENCE 236 AA; 25871 MW; BE01A28CD06EEE26 CRC64;
218
                                          197 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
179 LSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC
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                                                                                                                                                                                                                                                                                                                    236 AA
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InterPro; IPR003599; IG.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
InterPro; IPR003596; Ig_V.
Pfam; PF07654; C1-8et; I.
SWART; SW00407; IGC1; I.
SWART; SW00400; IG; I.
PROSITE; PS00359; IG_LIKE; I.
PROSITE; PS00290; IG_MHC; UNKNOWN_I.
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PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
                                          142 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 201
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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TISSUE=Lung;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; BC022362; AAH22362.1; -.
PIR; S22658; S22658.
PIR; S40324; S40324.
PIR; S40374; S40374.
PIR; S42267; S42267.
PIR; S42267; S42268.
HSSP; P01834; 1172.
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239 AA; 26234 MW; FACEDC3A3B03871D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                            184 TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
202 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236
                                                                                                                                                                                                                                                                                                                                                                                                                 239 AA
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PROSITE; PS00290; IG MHC; UNKNOWN 1.
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InterPro; IPR003597; 19_C1.
InterPro; IPR003006; 19_MHC.
InterPro; IPR003596; 19_V.
Pfam; PF07654; C1-8et; 1.
SMART; SM00406; IGV; 1.
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TISSUE=Lung;
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                                                                               VVTQES-ALTISPGETVTLICRSSIGAVTI--SNYANWVQEKPDHLFTGLIGGTNNRAPG
                                                         61 VPARFSGSLIGDKAALTITGAQTEDEARYFC---ALWYSCLWVFGGGTKLTVLSRTVAAP
                                                                                                                                                                             218
                                                                                                                                                                                             178 SLSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC
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7, 2005, 16:00:11

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

7, 2005, 15:28:46; Search time 114.5 Seconds (without alignments) 736.365 Million cell updates/sec. June Run on:

US-09-671-953B-7 1134 1 RSAVVTQESALTTSPGETVT......EVTHQGLSXPVTKSFNRGEC 218 Title: Perfect score: Sequence:

2105692 seqs, 386760381 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s: geneseqp2000s: geneseqp2011s: geneseqp2011s: geneseqp2013s: geneseqp2013s: geneseqp2013s: A_Geneseq_16Dec04: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description			•	_									Adl15445 Humanised	Ado00853 Humanised	Aae35326 Humanised	•			Adp79579 Chimeric	Aaw07528 Anti-HGF			_	Abu08018 Human mon	Adf65776 Human mon
SUMMARIES	;	QI .	AAB20360	AAB20359	AAB20358	ADQ98050	ADQ98051	ADR23362	AAE27925	ABB82834	ADL92471	AAW82740	AAB08025	AAE34878	ADL15445	AD000853	AAE35326	AAE34877	ADL15441	ADO00849	ADP79579	AAW07528	ADQ31891	ADQ31885	AA014066	ABU08018	ADF65776
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	& Query	Match	99.8	98.9	98.1	95.5	95.4	68.7	67.0	67.0	6.99	8.99	66.5	66.4	66.4	66.4	66.2	66.2	66.2	66.2	66.2	66.1	65.8	9.59	65.6	65.6	65.6
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ALIGNMENTS

Antibody engineering; metal chelate; CHA255; indium; EDTA; tumour; cancer; therapy; mutant; mutein. /label= FR2 /note= "framework region 2" 53. .59 /label= CDR2 /note= "complementarity determining region 2" "complementarity determining region 1" 'note= "complementarity determining region 3" note= "replaces Ser of wild-type sequence" Anti-chelate antibody CHA255 light chain mutant S95C. /note= "encoded by GTR" 101. .131 /label= FR4 /note= "framework region 4" l. .23 /label= FR1 /note= "framework region 1" /note= "framework region 3" 93. .100 /label= CDR3 'note= "encoded by CGW" 'note= "encoded by ACK" cocation/Qualifiers AAB20360 standard; protein; 218 AA. 24. .37 /label= CDR1 60. .92 /label= FR3 (first entry) 38..52 /label= F note= Misc-difference 100 Misc-difference 112 Misc-difference 113 Misc-difference 206 Misc-difference Mus musculus. Synthetic. 11-JUN-2001 AAB20360; Key Region Region Region Region Region Region Region RESULT 1

/note= "encoded by AGY"

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AAB20359;
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                         AAB20359
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                       /note= "encoded by TYG"
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                                                                                                                                        27-SEP-2000; 2000WO-US026619
                                                                                                                                                                               99US-0156194P
                                                                                                                                                                                                  31-MAY-2000; 2000US-0208684P
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Matches 218; Conservative
                                                                                                                                                                                                                                          (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                Chmura A;
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Misc-difference 207
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                                                            WO200122922-A2
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Nucleic acid encoding a mutant antibody comprising a reactive site that specifically binds to a metal chelate useful as analytical agents and in clinical diagnosis, as well as in the treatment of disease, particularly
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                                                                             engineering; metal chelate; CHA255; indium; EDTA; tumour;
                                                                                                                                                                                          "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                'note= "complementarity determining region 3"
                                                                                                                                                                                                                                                      "complementarity determining region 2"
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/note= "framework region 4"
                                                                                                                                                             "framework region 1"
                                                                                                                                                                                                                        "framework region 2"
                                                                                                                                                                                                                                                                                   region 3"
                                                           Anti-chelate antibody CHA255 light chain.
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/note= "framework
AAB20359 standard; protein; 218
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31-MAY-2000; 2000US-0208684P.
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/label= CDR3
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                                                                                                                                                                               label= CDR1
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|abel= FR1
                                       (first entry)
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/label=
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                                                                                        cancer; therapy
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                                                                                                           Mus musculus
                                       11-JJN-2001
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complementarity determining region (CDR) that specifically binds to a metal chelate against which the wild-type antibody is raised. The creative site of the mutant antibody is in a position proximate to or within the CDR, such that the chelate and the antibody are able to form a covalent bond. The present sequence is that of the light chain of anticovalent bond. The present sequence is that of the light chain of anticovalent bond. The present sequence is that of the light chain of anticovalent bond computer-aided design was used to develop an indium-EDTA chelate to covalently bind to CHA255 in vivo. The premise was to allow the chelate to bind non-covalently to CHA255 bound to a tumour and then to covalently attach the chelate to the antibody, thereby trapping it at the tumour site. This involved cloning the variable could be expressed in Escherichia coli, and the synthesis and screening of benzyl-EDTA chelates carrying weakly electrophilic groups capable of conjugation of the antibody in vivo. This Fab can be conjugated to a targeting moiety when desired. A reactive site was incorporated into the antibody by engineering a Cys residue at location Asn-96 or Ser-95 of the light chain, near the region of the antibody to which the chelate bound. This was accomplished by site-directed mitagenesis of a nucleic acid antibodies.
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98.9%; Score 1122; DB 4; Length 218;
Best Local Similarity 99.5%; Pred. No. 2.3e-78;
Matches 217; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibody engineering; metal chelate; CHA255; indium; EDTA; cancer; therapy; mutant; mutein.
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                                                                                                                                                                                                                                                                                                                                                     encoding the wild-type of the anti-chelate antibody
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/label= FR1
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/label= CDR2
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/label= FR2
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The invention provides a mutant antibody comprising a reactive site that is not present in the wild-type of the antibody. The antibody also has a complementarity determining region (CDR) that specifically binds to a metal chelate against which the wild-type antibody is raised. The complementarity determining region (CDR) that specifically binds to or within the CDR, such that the chelate and the antibody are able to form a covalent bond. The present sequence is that of the light chain variable contained bond. The present sequence is that of the light chain variable contained design was used to develop an indium-EDTA chelate to covalently bind to CHA255 in vivo. The premise was to allow the chelate to bind noncovalently to CHA255 bound to a tumour and then to covalently attach the covalently to CHA255 bound to a tumour and then to covalently attach the covalently to CHA255 bound to a tumour and then to covalently attach the covalently to CHA255 bound to a tumour and then to covalently attach the covalently and the spithesis and screening of CHA255 to construct a convalent contained to a transping it at the tumour site. This construct a nature of the antibody, thereby trapping it at the tumour site. This coll, and the spithesis and screening of CHA255 to construct a convalent could be expressed in Escherichia could, and the spithesis and screening of Denzyl-EDTA chelates carrying coll, and the spithesis and screening of penzyl-EDTA chelates carrying covic reactive site was incorporated into the antibody by engineering a Cys reactive site was incorporated into the antibody by engineering a Cys reactive site was incorporated into the antibody by site of the antibody to which the chelate bound. This was accomplished by site of the antibody to which the chelate bound. This was accomplished by site of the antibody to which the chelate bound. This was accomplished by site of the antibody to which the chelate bound and the coding the region of the antibody to which the relate belong the coding the coding the relate boun
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                                                        93. .100
/label= CDR3
/note= "complementarity determining region 3"
                                                                                                                                         note= "replaces Asn of wild-type sequence"
                                      'note= "framework region 3"
                                                                                                                                                                                                                                                   /note= "framework region
                                                                                                                                                                                                                                                                                              'note= "encoded by CGW"
                                                                                                                                                                                                                                                                                                                                         by ACK"
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31-MAY-2000; 2000US-0208684P.
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50. .92
/label= FR3
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N-PSDB; AAF30633.
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                                                                                                                                                                    Misc-difference 100
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  Region
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Score 1113; DB 4; Length 218; Pred. No. 1.1e-77;

98.1%; 99.1%;

Query Match Best Local Similarity

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                                                                          61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF 120
                                                                                        VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYSCLWVFGGGTKLTVLSRTVAAPSVF 120
                                                                                                                          IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
                                                                                                                                          IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180
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                                                                                                                                                                                                                                                                                                                                           Chimeric murine 2012.5 variable light chain fused to human TTCL protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vel mutant antibody comprising reactive site not present in wild-type antibody and antigen recognition domain that recognizes macrocyclic al chelate having four nitrogen atoms, useful for treating cancer or
                       RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG
                                               1 RSAVVIQESALTISPGETVILICRSSIGAVITSNYANWVQEKPDHLFTGLIGGTNNRAPG
                                                                                                                                                                                                                                                                                                                                                                   murine; mouse; chimeric; human; TTCL; tetanus toxin; magnetic resonance imaging; lanthanide luminescence; gamma-emissions; single photon emission tomography; SPET; cancer; cytostatic; immunosuppressive; multi-functional antibody; metal chelate; antigen recognition domain; in vivo imaging; cell-antibody-metal chelate complex; emission tomography.
 Gaps
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2; Indels
                                                                                                                                                                             STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                           STLTLSKADYEKHKVYACEVTHOGLSXPVTKSFNRGEC
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 41; SEQ ID NO 27; 208pp; English.
                                                                                                                                                                                                                                                                   ADQ98050 standard; protein; 218 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JAN-2003; 2003US-00350555.
22-JUL-2003; 2003US-00625047.
31-JUL-2003; 2003US-00631258.
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                                                                                                                                                                                                                                                                                                                  (first entry)
216; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Meares C, Corneillie T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-580725/56.
N-PSDB; ADQ98054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    autoimmune diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           musculus
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ADQ98050
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reactive functional group of the metal chelate. The present invention describes using these antibodies for in vivo imaging where the antibody comprises a targeting molety that binds specifically to a cell via a cell surface receptor or antigen thus forming a cell-mutant antibody complex. On addition of the metal chelate, a cell-antibody-metal chelate complex. Is formed that can be detected using emission tomography, magnetic resonance imaging, lanthanide luminescence, gamma-emissions or single photon emission tomography (SPET). As such, this method is useful for treating a subject with cancer and pharmaceutical compositions exhibit cytostatic and immunosuppressive activities. This polypeptide sequence is the chimeric mutine antibody 2012.5 variable light chain protein fused to the human anti-tetanus toxin antibody kappa light chain constant region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RSAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGNNNRPPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mouse; chimeric; human; TTCL; tetanus toxin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1083; DB 8;
Pred. No. 2.3e-75;
0; Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.5%;
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22-JUL-2003; 2003US-00625047.
31-JUL-2003; 2003US-00631258.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 95.9
Matches 209; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 218 AA;
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Chimeric.
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Homo sapiens

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chelating agents and metal chelates, particularly macrocyclic metal chelates. Specifically, it refers to an antibody that comprises a metal chelates becidically, it refers to an antibody that comprises a metal chelate bound to an antigen recognition domain, where the metal chelate chelate bound to an antigen recognition domain, where the metal chelate cactive site of the antibody. This reactive site is the side chain of a reactive site of the antibody. This reactive site is the side chain of a caturally occurring amino acid e.g. the -SH group side chain of a caturally occurring amino acid e.g. the -SH group side chain of a covalent bond between the reactive site of the antibody and the a covalent bond between the reactive site of the antibody and the cactive functional group of the metal chelate. The present invention cantiger exceptor or antigen thus forming a cell-mutant antibody complex. On addition of the metal chelate, a cell-antibody-metal chelate complex is formed that can be detected using emission tomography, magnetic resonance imaging, lanthanide luminescence, gamma-emissions or single photon emission tomography (SPET). As such, this method is useful for treating a subject with cancer and pharmaceutical compositions exhibit cytostatic and immunosuppressive activities. This polypeptide sequence is the chimeric mutant N33C murine antibody 2D12.5 variable light chain
                                                                                                                                                                       el mutant antibody comprising reactive site not present in wild-type antibody and antigen recognition domain that recognizes macrocyclic al chelate having four nitrogen atoms, useful for treating cancer or
                                                                                                                                                                                                                                                                                                                                                            invention relates to multi-functional antibodies that recognise
                                                                                                                                                                                                                                                                                                       Claim 41; SEQ ID NO 28; 208pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     constant region of the invention.
(REGC ) UNIV CALIFORNIA
                                                  Corneillie
                                                                                                     2004-580725/56.
                                                                                                                                                                                                                                                       autoimmune diseases
                                                                                                                               N-PSDB; ADQ98055
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                                                       Meares C,
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Gaps . Score 1082; DB 8; Length 218; Pred. No. 2.7e-75; 0; Mismatches 9; Indels (95.4%; ilarity 95.9%; Conservative 0 Local Similarity ses 209; Conserv Query Match Best Loca Matches

1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG

à

I PPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS 180 120 VPARFSGSIIGDKAALTIAGTQTEDEAIYFCALWYSNHWVFGGGTKLTVLSRTVAAPSVF 120 9 RSAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGCNNRPPG VPARFSGSLIGDKAALTITGAQTEDEARYFCALMYCNLWVFGGGTKLTVLSRTVAAPSVF STLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218 61 121 181 g ð 셤 ò 셤 ઠ 셤

RESULT 6 ADR23362

ADR23362 standard; protein; 215

ADR23362;

04-NOV-2004 (first entry)

Human CD72-targeted IgG1 light chain. XXXXXXXXXXXX

Human, CD72, B-lymphocyte; receptor; scFv; antibody; cytostatic; immunosuppressive; cancer; autoimmune disease; gene therapy.

New internalizing human binding molecules capable of specifically binding to CD72, useful for diagnosing and/or treating B-cell associated diseases, such as cancer or autoimmune disorders. Example 5; SEQ ID NO 54; 174pp; English Location/Qualifiers 1. .109 /label= V_region 110. .215 /label= C_region 27-JAN-2003; 2003WO-EP050004 27-JAN-2003; 2003WO-EP050004 (CRUC-) CRUCELL HOLLAND BV. Bakker ABH, Marissen WE; 2004-580978/56. N-PSDB; ADR23361. WO2004067569-A1 Region Region Key

The present sequence is the protein sequence to the injuriant of antigen CD72. An acry was shown to specifically recognises human B cell associated antigen CD72. An acry was shown to specifically recognise the human CD72 receptor. The acry was recloned in IgG expression vector C01 using primers designed to restore complete human frameworks, thereby generating antibody 025. Such anti-CD72 immunoglobulins or their antigen-binding fragments can be used as internalising human binding molecules of the invention. These internalising human binding molecules of the invention. These conternalising human binding molecules of the invention to the surface of binding to CD72 or its antigenic determinant, and preferably bind to CD72 binding to CD72 present on the surface of casociated with cells. Upon binding to CD72 present on the surface of trarget cells, the binding molecules, the invention provides internalising human binding molecules, the invention provides comprising an internalising mean of casociated with compositions compositions compositions compositions composition of internalising human binding molecule, immunoconjugate, nucleic acids encoding these, and compositions comprising them. The internalising human binding molecule, immunoconjugate, nucleic acids encoding these, and compositions composition can be used in the diagnosis and/or treatment of a B cell associated disorder or disease, especially a B cell associated cancer and B cell associated autoimmune disorder (claimed). present sequence is the protein sequence of the light chain of

Sequence 215 AA;

4 111 174 61 57 AAPSVF1FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD SAVVTQESALTISPGETVILTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGV PARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNL-----WVFGGGTKLTVLSRTV Gaps 31; Indels 16; Length 215; STYSLSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218 Query Match
Best Local Similarity 72.3%; Pred. No. 5.4e-52;
Matches 162; Conservative 15; Mismatches 31; 62 115 175

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to domain deleted CC49 or C2BB antibodies.

Domain deleted CC49 antibodies comprise a heavy chain human CC49 domain deleted sequence in which CL12 domain has been deleted and are reactive with tumour associated antigen (TAG)-72. The C2BB antibodies are reactive with tumour associated antigen (TAG)-72. The C2BB antibodies are reactive with CD20 and comprise a heavy chain having a sequence of a derived domain deleted C2BB construct where the CH2 domain has been deleted.

Sequences of the invention are useful for imaging a neoplasm. They are also useful for treating myelosuppressed patients suffering from neoplastic disorder such as haematologic neoplasm, preferably non-coplastic disorder, colon cancer and haematologic malignancy. They are useful for reducing tumour size, inhibiting tumour growth and/or treating tumours. The present sequence is human C2BB light chain protein. This sequence is used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel domain deleted CC49 antibody reactive with tumor associated antigen -72, or C2B8 antibody reactive with CD20, useful for treating myelosuppressed patient suffering from a neoplastic disorder.
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                                                                                                                                                                              Human, CC49 antibody, C2B8 antibody, tumour associated antigen, TAG-72, neoplasm, neoplastic disorder, haematologic neoplasm, colon cancer, non-Hodgkin's lymphoma, haematologic malignancy, tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSAVVIQES -- ALTISPGETVILICRSSIGAVITISNYANWVQEKPDHLFIGLIGGINNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 RGQIVLSQSPAILSASPGEKVTMTCRAS----SSVSYIHWFQQKPGSSPKPWIYATSNLA
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                                                                                                                                            Human C2B8 antibody light chain protein.
                                 AAE27925 standard; protein; 235 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chinn P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 3B; 74pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               29-JAN-2001; 2001US-0264318P.
16-NOV-2001; 2001US-0331481P.
                                                                                                                                                                                                                                                                                                                                                              29-JAN-2002; 2002WO-US002373
                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanna N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IDEC-) IDEC PHARM CORP.
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N-PSDB; AAD45754.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Braslawsky GR,
                                                                                                                                                                                                                                                                                      WO200260955-A2
                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                          27-DEC-2002
                                                                                                                                                                                                                                                                                                                          08-AUG-2002
                                                                       AAE27925;
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Matches
RESULT 7
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monomeric subunits, where the monomeric subunits are non-covalently associated. (I) is useful for treating a disorder, especially immune disorder, and neoplastic disorder such as relapsed Hodgkin's disease.

resistant Hodgkin's disease high grade, low grade and intermediate grade non-Hodgkin's lymphomas. B cell chronic lymphocytic leukemia (B-CLL). lymphoplasmacytoid lymphoma (LPL), mantle cell lymphoma (MCL), follicular lymphoma (EL), diffuse large cell lymphoma (DCL), Burkitt's lymphoma (BCL), diffuse large cell lymphoma, angioimmunoblastic lymphoma (BCL), and lymphocytic, follicular, diffuse large cell, diffuse small cleaved cell, and non-Burkitt's follicular, mixed small cleaved burkitt's and non-Burkitt's follicular, mixed small cleaved cell lymphomas, in a mammal (see ABZ24017 for a represents the antibody C2B8 light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel dimeric antibody useful for treating immune disorder and neoplastic disorder, has several non-covalently associated monomeric subunits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 SGVPVRFSGSGSGTSYSLTISRVEAEDAATYYCQQWTSNPPTFGGGTKLEI-KRTVAAPS 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C2B8; antibody; cytostatic; antiallergic; antianemic; antiasthmatic; vsotropic; immunomodulator; protozoacide; antidiabetic; nephrotropic; thyromimetic; hepatotropic; haemostatic; antileprotic; antibacterial; neuroprotective; antipsoriatic; antirheumatic; antiantic; antiulcer; dermatological; immunosuppressive; antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 RGQIVLSQSPAILSASPGEKVTMTCRAS----SSVSYIHWFQQKPGSSPKPWIYATSNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RSAVVIQES -- ALTISPGETVILICRSSIGAVITSNYANWVQEKPDHLFTGLIGGINNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a dimeric antibody (I) comprising several
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chinn P, Hariharan K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67.0%; Score 759.5; DB 6
70.5%; Pred. No. 1.9e-50;
ive 16; Mismatches 42
                                                                                                                                                                                                          Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Fig 3B; 78pp; English.
                                                                                                                                                                                                          ABB82834 standard; protein; 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JAN-2001; 2001US-0264318P.
16-NOV-2001; 2001US-0331481P.
21-DEC-2001; 2001US-0341858P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-2002; 2002WO-US002374.
                                                                                                                                                                                                                                                                                                                                                                                                                    chain.
                                                                                                                                                                                                                                                                                                                                             31-MAR-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Braslawsky GR, Hanna N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IDEC-) IDEC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2003-140446/13.
                                                                                                                                                                                                                                                                                                                                                                                                            Antibody C2B8 light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 155; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABZ24018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200296948-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-DEC-2002
                                                                                                                                                                                                                                                                             ABB82834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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ARFSGSGSTSYSLTISRVEAEDAATYYCQHWSSKPPTFGGGTKLEI-KRTVAAPSVFIF 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence is used in a method for obtaining a novel gene construct (A) which expresses, in cells of a mammal, a conjugate (B) of a cell-targeting group (I) and a heterologous prodrug-converting enzyme (II), and (B) is directed to leave the cell for selective localisation at a cell surface antigen (Ag) recognised by (I). Delivery of (A) to a target site, then administration of (III) is used for targeted release of cytotoxic drug, specifically for treating cancer but also inflammation such as rheumatoid arthritis. In situ generation of the targeting antibody increases selectivity, reducing side effects at normal tissue. The method is applicable to any antibody-directed enzyme prodrug therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New gene construct expressing conjugate of targetting agent and prodrug-
converting enzyme - useful for, e.g. targetted production of cytotoxic
drug in vivo, especially for treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARESGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                          Conjugate; cell targeting; cytotoxic drug; prodrug therapy system; prodrug-converting enzyme; cell surface antigen; treatment; cancer; inflammation; rheumatoid arthritis; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.8%; Score 757; DB 2; Length 235; 71.8%; Pred. No. 3e-50; ive 15; Mismatches 40; Indels
                                                                LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC
                                                                                                                                                                                                                                                                                              Plasmid pNG3/A5B7VK-HuCK-NEO protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1f; Page 70; 100pp; English
                                                                                                                                                                              AAW82740 standard; protein; 235 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-GB001294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97GB-00009421
                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Emery SC, Blakey DC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-059700/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAV72047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9851787-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAY-1998;
                                                                                                                                                                                                                                                        10-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Sim
Matches 155;
                                                                                                                                                                                                                                                                                                                                    Conjugate;
                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123
                                                                                                                                                                                                                  AAW82740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
          118
                                            183
                                                                                  178
                                                                                                                                                                AAW82740
                                                                                                                                          RESULT
                                                                                                                                                                                                  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
          셤
                                            ઠે
                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 ARFSGSLIGDKAALTIIGAQTEDEARYFCALWYCNLWVFGGGTKLIVLSRTVAAPSVFIF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 PPSDEQLKSGTASVVCLLANFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
                                                136 VFIFFPFSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an antibody comprising an Fc variant portion having an amino acid modification in the Fc region of the parent Fc polypeptide, where the Fc variant modulates binding to an Fc-gamma-R compared to the parent Fc polypeptide. The antibody may also be used in research and in agricultural or industrial applications. This sequence corresponds to the light chain of the antibody "Rituximab" as an example
                                                                                                                                                                                                                                                                                                                                                                                                antiinflammatory; cardiovascular; gene therapy; antibody; Fc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 VLSQSPAILSASPGEKVTWTCRAS----SSVSYIHWFQQKFGSSPKFWIXATSNLASGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New optimized Fc variant antibody useful for diagnosing or treating diseases (e.g. cancer, inflammation or cardiovascular diseases), in research and in agricultural or industrial applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Doberstein SK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66.9%; Score 759; DB 8; Length 213; 71.8%; Pred. No. 1.9e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39; Indels
                                                                                                                            196 LSSTLTLSKADYERGHKVYACEVTHOGLSSPVTKSFNRGEC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Desjarlais JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16; Mismatches
                                                                                                                                                                                                                                                                                                                                                          Antibody "Rituximab" light chain sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 12; Fig 31a; 192pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                    agriculture; industrial application
                                                                                                                                                                                                                                            Ė
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an antibody of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dang W,
Vafa O;
                                                                                                                                                                                                                                            ADL92471 standard; protein; 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-2002; 2002US-0414433P.
23-JAN-2003; 2003US-0442301P.
02-MAY-2003; 2003US-0467606P.
12-JUN-2003; 2003US-0477639P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-SEP-2003; 2003WO-US030249
                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chirino AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Karki SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-316096/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 155; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 213 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2004029207-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (XENC-) XENCOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                        01-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                    cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lazar GA,
Hayes RJ,
                                                                                                          179
                                                                                                                                                                                                                                                                                  ADL92471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
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dermatitis, Crohn's disease, Graves's disease,
                                                                                                                                                                                                                                                                                            Sequence 235 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200294879-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                           Best Local Sim:
Matches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59
                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE34878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE34878
ID AAE3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement system; Fcgamma receptor; cytotoxic effector cell; boost immune cell; programmed cell death; allergic disorder; cancer; autoimmune disease; allergic asthma; atopic dermatitis; Crohn's disease; allergic bronchopulmonary aspergillosis; allergic rhinitis; Graves's disease; food allergy; allergic contact dermatitis; cancer; becall imphoma; rheumatoid arthritis; ulcerative colitis; psoriasis; pigeon breeder's disease; hepatitis; leprosy; Lyme disease; disease; aplastic anaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "murine anti-human CD20 variable light chain"
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129. .235
/note= "human kappa light chain constant region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anti-CD20 antibody; dimeric immunoglobulin; immunoglobulin; IgG;
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                                                                   LTLSKADYEKHKVYACEVTHOGLSXPVTKSFNRGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A dimeric anti-CD20 light chain polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "signal peptide"
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                                                                                                                                                                                                                                                       AAB08025 standard; protein; 235 AA
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                                                                                                                                                                                                                                                                                                                                                                                        (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHARM CORP
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Homo sapiens.
Chimeric.
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14-NOV-2000
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                              183
                                                                                           200
                                                                                                                                                                                                                                                                                                                           AAB08025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
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allergic contact dermatitis, CLL cancers and/or B-cell lymphomas. They may also be used to treat a range of other diseases and disorders such as rhemmatoid arthritis, ulerative colitis, psoriasis, pigeon breeder's disease, hepatitis, leprosy, Lyme disease, diabetes mellitus, candidiasis and aplastic anaemia. They are also useful for inducing hyper-cross-linking of membrane antigens and for the preferential killing of selected cell populations. (Updated on 12-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BIWA8 antibody; heavy chain variable region; light chain variable region; VH; VL; CD44v6; medicament; cancer; antibody therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to novel antibody molecules comprising a variable region of the heavy (VH) and/or light chain (VL) of CD44v6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 RGQIVLSQSPAILSASPGEKVTMTCRAS----SSVSYIHWFQQKPGSSPKRWIYATSNLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VFI FPPSDEQLKSGTASVVCLLNNFY PREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RSAVVTQES -- ALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRA
                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                    66.5%; Score 754.5; DB 3; Length 235; 70.0%; Pred. No. 4.6e-50; ive 16; Mismatches 43; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heider K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIWA4/8 antibody light chain mature protein.
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26-SEP-2001; 2001US-0325147P.
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N-PSDB; AAD53214, AAD53217.
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Ношо
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specific humanised antibody called BIWA8 and BIWA4. Sequences of the invention are useful for manufacturing a medicament and for treating cancer including colorectum, non-small cell lung, breast, head and neck, ovariam, lung, bladder, pancreatic cancer or metastatic cancers of the brain. They are also useful in antibody therapy. The present sequence is BIWA4/8 antibody light chain mature protein. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                117
                                                                                                                                                                                                                                        182
                                                                                                                                                                                                                                                           177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of a conjugate of antibody to specified cell differentiation antigen with cytotoxic compound in the preparation of pharmaceutical composition for the treatment of cancer.
                                                                                                                                                    62
                                                                                                                                                                       58
                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer; cell differentiation antigen-44; CD44; cytotoxic; chemotherapeutic agent; cytostatic; head; neck squamous cell carcinoma; oesophagus; lung; skin; cervix; breast adenocarcinoma; pancreas; colon; stomach; human; murine; mouse; antibody; BIWAB; light chain.
                                                                                                                                                                                                         PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST
                                                                                                                                                                ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF
                                                                                                                                                                                                                                      PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST
                                                                                                                                                   4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel method for the preparation of a pharmaceutical composition for the treatment of cancer whereby a conjugate of a specific antibody to cell differentiation antigen-44
                                                                                                                               9
                                                                                                          Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                         Humanised murine antibody BIWA8 light chain protein.
                                                                                                                               40;
                                                                                                                                                                                                                                                                                            66.4%; Score 753; DB 6; 72.2%; Pred. No. 5.4e-50;
                                                                                                                                                                                                                                                                                 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC
                                                                                                                                14; Mismatches
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                                                                                                                      Best Local Similarity 72.2%
Matches 156; Conservative
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                                                                                       Sequence 213 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPSDEQLKSGTASVVCLLNNPYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28
chemotherapeutic agent. The method of the invention has cytostatic chemotherapeutic agent. The method of the invention has cytostatic chemotherapeutic agent. The method of the invention has cytostatic compositions and may be useful in the preparation of a pharmaceutical composition for the treatment of cancer, particularly head and neck aquamous cell carcinoma, estin squamous cell carcinoma, skin squamous cell carcinoma, skin squamous cell carcinoma, skin squamous cell carcinoma, breast adenocarcinoma, lung adenocarcinoma, pancreas adenocarcinoma, colon adenocarcinoma and stomach adenocarcinoma. The current sequence is that of the humanised murine antibody BIWAB light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPSDEQLKSGTASVVCLLINFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 VLTQSPATLSLSPGERATLSCSAS----SSINYIYWLQQKPGQAPRILIYLTSNLASGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 ARPSGSGSGTDFTLTISSLEPEDFAVYYCLQWSSNPLTFGGGTKVEI-KRTVAAPSVFIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CD44 specific antibody; CD44; cancer; radiotherapy; CD44v6 specific antibody; maycansinoid; radioimmunotherapeutic; cytostatic; immunostimulator; head and neck squamous cell carcinoma; oesophagus squamous cell carcinoma; lung squamous cell carcinoma; lung squamous cell carcinoma; skin squamous cell carcinoma; breast adennocarcinoma; lung adenocarcinoma; pancreas adenocarcinoma; breast adenocarcinoma; semach adenocarcinoma; pancreas adenocarcinoma; colon adenocarcinoma; stomach adenocarcinoma; humanised murine antibody BIWA 8 light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Humanised murine antibody BIWA 8 light chain protein SEQ ID NO:8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 753; DB 8; Length 213;
; Pred. No. 5.4e-50;
14; Mismatches 40; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BOEH ) BOEHRINGER INGELHEIM INT GMBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ŕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADO00853 standard; protein; 213
                                                                                                                                                                                                                                                                                                            chain protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-NOV-2002; 2002EP-00024881
                                                                                                                                                                                                                                                                                                                                                                                                                                        66.4%;
72.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 72.2
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-378705/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AD000854
                                                                                                                                                                                                                                                                                                                                                                        Sequence 213 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUL-2004
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moiety
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Sproll M;

Patzelt E,

Heider K,

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63 ARFSGSLIGDKAALTITGAQTEDBARYFCALMYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a compound comprising CD44 specific antibody molecule conjugated to a highly cytotoxic drug, which cleaves under intracellular conditions. The compound is used in pharmaceutical composition for the treatment of cancer, solid tumours, and as an adjuvant to surgical intervention to treat minimal residual disease. The present sequence is humanised murine antibody BIWA4 light chain protein
                                                                                                                                                                                                                                                                                                                                                                                                                                     New compound useful for treatment of cancer comprises CD44 specific antibody molecule conjugated to a highly cytotoxic drug, which cleaves under intracellular conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST
                                                                                                                                                                                                                    (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Page 14; 31pp; English
                                                                                           18-MAY-2001; 2001EP-00112227.
                                                                                                                                                         18-MAY-2001; 2001EP-00112227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used in the invention
                                                                                                                                                                                                                                                                                                                                             WPI; 2003-177273/18.
N-PSDB; AAD53976.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 213 AA;
                             20-NOV-2002
                                                                                                                                                                                                                                                                                  Adolf G,
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                                                                           The present invention describes using a compound (CD) of formula A(LB)n, where A is an antibody molecule which is specific for CD44, L is a linker molecy. B is a compound which is toxic to cells, and n is a decimal number between 1-10, for the preparation of a pharmaceutical composition for the treatment of cancer, where CD is used or is for use in combination with radiotherapy. Also described: (1) use of a conjugate (CJ) of a CD44v6 specific antibody molecule and a maytansinoid for the manufacture of a pharmaceutical composition for the treatment of cancer, where CJ is used or is for use in combination with radiotherapy; (2) a pharmaceutical composition for the treatment of cancer, where CD is used or is for use in comprising CD or CJ rogether with a radioimmunotherapeutic agent and optionally further comprising on or more carrier(s), diluent(s), or excipient(s); (3) a kit comprising in a composition for the preparation of a pharmaceutical composition for the cradioimmunotherapeutic agent; and (4) use of radioimmunotherapeutic agent; and (4) use of radioimmunotherapeutic agent; of a pharmaceutical composition for the cradioimmunotherapeutic agent; where the radioimmunotherapeutic agent is used or is consument of anner, where the radioimmunotherapeutic agent is used or is consument of amedicament for the treatment of cancer, where the radioimmunostimulators. CJ is useful for the squamous cell carcinoma, breast adenocarcinoma, lung adenocarcinoma, pancreas adenocarcinoma, colon adenocarcinoma, lung adenocarcinoma, pancreas adenocarcinoma, colon adenocarcinoma, lung adenocarcinoma, pancreas adenocarcinoma, into adenocarcinoma, and stoment of cancer. CD and CJ are useful for treating cancer in a compination with radiotherapy. CD and CJ are useful as an adjuvant to surgical interaction, to treat minimal residual disease. The present compination with radiotherapy, CD and CJ are useful disease. The present compination in the axemplification of a parageral interaction, to treat minimal residual disease. The present is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>ښ</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
66.4%; Score 753; DB 8;
Best Local Similarity 72.2%; Pred. No. 5.4e-50;
Matches 156; Conservative 14; Mismatches 40
                             7; SEQ ID NO 8; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 213 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123
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118 PPSDEQLKSGTASVVCLLINNFYPREAKVOWKVDNALQSGNSQESVTEQDSKDSTYSLSST 177
                                         LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                              Search completed: June
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                                                                                                                                                                LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                     LTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 213
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CD44; cytotoxic drug; therapy; cancer; tumour; minimal residual disease; antigen; cytostatic; BIWA4 antibody; murine.

Homo sapiens EP1258255-A1

Humanised murine antibody BIWA4 light chain protein.

(first entry)

17-JUN-2003

ZXSXZZXZXXXX ZXSXZZXZXXXX

AAE35326;

AAE35326 standard; protein; 213 AA

AAE353

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7, 2005, 15:54:04
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182

58

Gaps

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4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP

66.2%; Score 751; DB 6; Length 213; 72.2%; Pred. No. 7.6e-50; rive 13; Mismatches 41; Indels

Similarity

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Query Match 66.8%; Score 757; DB 3; Length 235; Best Local Similarity 71.8%; Pred. No. 7.9e-67; Matches 155; Conservative 15; Mismatches 40; Indels
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                                                                                                                                                                                                                                                      7, 2005, 15:42:01; Search time 29.5 Seconds (without alignments) 551.644 Million cell updates/sec
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Sequence
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        5.1.6
Compugen Ltd
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US-08-952-235-1
US-09-669-971-1
US-09-472-087-67
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US-09-011-769A-27
US-09-472-087-69
US-09-472-087-17
US-09-472-087-19
US-09-472-087-14
US-09-472-087-14
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US-09-456-090A-84
US-09-456-090A-86
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US-09-456-090A-86
US-09-456-090A-86
US-09-456-090A-46
US-09-458-234-46
US-09-448-516-12
US-09-448-516-12
US-09-448-516-12
US-09-438-234-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
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GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                               sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                               protein search, using
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seq length: 200000000
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1134
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Sequence 74, Appl Sequence 69, Appl Sequence 67, Appl Sequence 5, Appli Sequence 6, Appli Sequence 72, Appl Sequence 72, Appl Sequence 72, Appl Sequence 74, Appl Sequence 56,	
28 722.5 63.7 226 4 US-09-453-234-74 29 722 63.7 233 3 US-09-485-7378-69 30 722 63.7 233 4 US-09-485-7378-69 31 721.5 63.6 238 1 US-08-1152-2 32 721.5 63.6 238 1 US-08-1152-2 33 720.5 63.5 213 3 US-08-157-101A-5 34 720.5 63.5 213 3 US-09-273-463-6 35 719 63.4 219 3 US-09-273-449-72 36 719 63.4 219 3 US-09-274-3647-72 37 719 63.4 219 4 US-09-171-952A-72 38 719 63.4 242 3 US-09-024-449-56 41 719 63.4 242 3 US-09-024-444-56 42 719 63.4 242 3 US-09-024-444-56 43 719 63.4 242 3 US-09-024-444-56 44 719 63.4 242 3 US-09-024-952A-56 45 718 63.4 242 3 US-09-024-952A-56 46 718 63.4 242 3 US-09-024-344A-56 47 718 63.4 242 3 US-09-024-344A-56 48 718 63.4 242 3 US-09-024-344A-56 49 718 63.4 242 3 US-09-121-952A-56 49 718 63.4 242 3 US-09-121-952A-56	RESULT 1 US-09-423-439-18 US-09-423-439-18 Sequence 18, Application US/09423439 Patent No. 633970 GENERAL INFORMATION: APPLICANT: EMERY, Stephen Charles TITLE OF INVENTION: CHEMICAL COMPOUNDS NUMBER OF SEQUENCES: 60 CORRESPONDENCE ADDRESS: ADDRESSEE: Pillsbury Winthrop, L.L.P. STATE: 100 New York Ave., N.W. CITY: Washington STATE: D.C. COUNTRY: U.S.A. INPOUNTRY: U.S.A. APPLICATION NEWBER: POSY/MS-DOS SOFTWARE: ME PODS/MS-DOS SOFTWARE: ME NOTOW: CHAROW: CURRENT APPLICATION NUMBER: CT/GB98/01294 FILING DATE: 09-No. 6339070-1999 CIASSIFICATION NUMBER: RB 9709421.3 PRIOR APPLICATION NUMBER: RB 9709421.3 FILING DATE: 10-MAY-1997 INFORMATION POR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS: LENGTH: 335 amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: procein SEQUENCE DESCRIPTION: SEQ ID NO: 18: US-09-423-439-18

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Gaps

9

ARESGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGCTKLTVLSRTVAAPSVFIF 122

63

VVTQESA-LITISPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP

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US-09-669-971-1
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                                                        140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199
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81 ARFSGSGSGTSYSLTISRVEAEDAATYYCQHWSSKPPTFGGGTKLEI-KRTVAAPSVFIF 139
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                                                                                                                                                                                                                                                                                 APPLICANT: Schwall, Ralph H.
APPLICANT: Schwall, Ralph H.
APPLICANT: Tabor, Kelly H.
TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
TITLE OF INVENTION: Antagonists and Uses Thereof
NUMBER OF SEQUENCES: 4
NUMBER OF SEQUENCES: 4
NUMBER OF SEQUENCES: 4
NUMBER OF SEQUENCES: 4
STREET: 1 DNA Way
CITY: South San Francisco
STATE: Galifornia
COUNTRY: USA
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                                                                                                              183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                  66.1%; Score 750; DB 3; 71.8%; Pred. No. 3.6e-66; iive 13; Mismatches 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94080
COMPUTER READABLE FORM:
COMPUTER: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genenterh)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/460368
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0938P1
TELECOMMUNICATION INFORMATION:
TELECPHONE: 650/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,235
                                                                                                                                                                                                                                                 Sequence 1, Application US/08952235 Patent No. 6207152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 220 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 71.8
Matches 153; Conservative
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SGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFPPS 125
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                                                                                    APFLICANT: Schwall, Ralph H.
Tabor, Kelly H.
TITLE OF INVENTION: Heparcoyte Growth Factor Receptor
Antagonists and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/952,235
FILING DATE: «UDKNOWN>
APPLICATION NUMBER: 08/460368
FILING DATE: 02-UN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/669,971
FILING DATE: 05-Jul-2001
CLASSIFICATION: <unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0938P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                   CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
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US-09-472-087-15
; Sequence 15, Application US/09472087
; Patent No. 6682736
Sequence 1, Application US/09669971; Patent No. 6468529; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 220 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 71.8%
Matches 153, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: Amino Acid
                                                                                                                                                                                              NUMBER OF SEQUENCES:
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64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFP 123
                                                                                                                                                                           123 PPSDEQLKSGTASVVCLLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
                                                                                                                                                                                                                                                                                                               5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA
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4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
                                                                                                                                    63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF
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4.2e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: One Market Plaza, Steuart Tower, Suite 2000 CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Weiner, George
APPLICANT: Gingrich, Roger
APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Bispecific Antibody Effective tritle OF INVENTION: B-Cell Lymphoma and Cell Line
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397,411
                                                                                                                                                                                                                                                                                                                                                                                                                183 LTLSKADYEKHKVYACEVTHOGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Townsend and Townsend and Crew
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        011823-004901
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FILING DATE: 01-MAR-1995
CLASIPITCATION: 424
PRIOR APPLICATION: 427
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/859,583
FILING DATE: 27-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFECCHANDICATION NUMBER: 30,1223
REFECCHANDICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/08397411; Patent No. 6129914; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 213 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 70.7%
Matches 152; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415-326-2422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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US-08-397-411-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
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APPLICANT: HANSON, DOUGLAS C.
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: MEVEU, MARK J.
APPLICANT: MEVEU, MARK J.
APPLICANT: MEVEU, MARK J.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX -PF1
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 05/113,647
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR PLILNG DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 67
LENGTH: 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65.5%; Score 743; DB 4; Length 233; 70.4%; Pred. No. 1.9e-65; ive 19; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 65.5%; Score 743; DB 4; Length 23
Best Local Similarity 70.4%; Pred. No. 1.9e-65;
Matches 152; Conservative 19; Mismatches 39; Indels
                                APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, BILLER E.
APPLICANT: HANKE, JEFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GORVALAN, JOSE R.
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX.PF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-112-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 233
TYPE: PRT
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Patent No. 6682736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-09-472-087-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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Best Local Similarity
Matches 152; Conserv
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US-09-472-087-67
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Sequence 79, Application US/09315926A

Patent No. 6498027

GENERAL INFORMATION:

APPLICANT: Bavan, Helmuth

APPLICANT: Havenga, Menzo

APPLICANT: Havenga, Menzo

APPLICANT: Havenga, Menzo

APPLICANT: Werlinder, Seefan

TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER

FILE REFERENCE: 2183-4080US

CURRENT APPLICATION NUMBER: EP 99201593.3

PRIOR FILING DATE: 1999-05-20

PRIOR FILING DATE: 1999-05-20

PRIOR FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 81

SOCTHARE: PATENT VERSION 3.0

SEQ ID NO 79

LENGTH: 236
71 GDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFPPSDEQLK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GADFTLINKLEPEDFAVYYCQRYGRSLWTFGQGTKVEIKRGTVAAPSVFIFPPSDEQLK 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPARFSGSLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
OTHER INFORMATION: Description of Artificial Sequence: phage
NAME/KEY: PEPTIDE
LOCATION: (1)..(236)
OTHER INFORMATION: /note="hCAT1 amino acid sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.7%; Score 734; DB 4; Length 236; 72.6%; Pred. No. 1.5e-64; Live 14; Mismatches 41; Indels
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APPLICANT: HANSON, DOUGLAS C.

APPLICANT: HAUSON, MARK J.

APPLICANT: MUELLER, BILLEN E.

APPLICANT: HANKE, JEFREY H.

APPLICANT: GILMAN, STEVEN C.

APPLICANT: GILMAN, STEVEN C.

APPLICANT: CORVALAN, JOSE R.

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4

FILE REFERENCE. ABX-PPI
                                                                   183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                            200 LTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 72.68 Matches 151; Conservative
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63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 VLTQSPSSLSVSVGDRVTMTCRAS----SSVTYIHWYQQKPGLAPKSWIYATSNLASGVP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.9%; Score 736; DB 4; Length 235; llarity 70.8%; Pred. No. 9.4e-65; Conservative 15; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

ZIP: 20005

COMPUTER: EDABLE FORM:

MEDIUM TYPE: 1.44 Mb disk

COMBUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/011,769A

FILING DATE: 13-Feb-1998

CLASSIFICATION: «Unknown>
PRIOR APPLICATION NUMBER: PCT/GB96/01975

FILING DATE: 13-AUG-1996

APPLICATION NUMBER: GB 9612295.7

FILING DATE: 12-JUN-1996

APPLICATION NUMBER: GB 961019.2

FILING DATE: 12-MAY-1996

APPLICATION NUMBER: GB 9516810.0

FILING DATE: 16-AUG-1995

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 235 amino acids
                                                                                                                                                      184 TLSKADYEKHKVYACEVTHOGLSXPVTKSFNRGEC 218
                                                                                                                                                                                    179 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Pillabury Madison & Sutro,
STREET: 1100 New York Ave., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              HENNEQUIN, CLUTENT F.A.
MARSHAM, Peter R.
DOWELL, Robert I.
TITLE OF INVENTION: Chemical Compounds
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-011-769A-27
                                                                                                                                                                                                                                                                                                          Sequence 27, Application US/09011769A
Patent No. 6436691
GENERAL INFORMATION:
APPLICANT: SLATER, Anthony M.
BLAKEY, David C.
DAVIES, David H.
HENNAM, John F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 153; Conserv?
                                                                                                                                                                                                                                                                   RESULT 7
US-09-011-769A-27
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140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199
139 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 198
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GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: WUELLER, ELLENE E.
APPLICANT: MUSILER ELLENE E.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GORVEREY H.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PF1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PATENTIN OF: 2.1
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APPLICANT: HANSON, MARK J.
APPLICANT: MUSELLER, EILLEN E.
APPLICANT: MUSELLER, EILLEN E.
APPLICANT: GLIAMA, STEVEN C.
APPLICANT: GLIAMA, STEVEN C.
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PF1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR PELING DATE: 1999-12-23
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                                                                                            183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC
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                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 14, Application US/09472087; Patent No. 6682736
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Matches 150; Conservative
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ORGANISM: Homo sapiens
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US-09-472-087-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
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APPLICANT: HANSON, DOUGLAS C.
APPLICANT: WUELLER, ELLLER E.
APPLICANT: WUELLER, ELLLER E.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: GILMAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PP1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR PILING DATE: 1998-12-23
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Pred, No. 2.1e-64;
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Best Local Similarity 69.9%; Pred. No. 2.1e-
Matches 151; Conservative 18; Mismatches
                          CURRENT APPLICATION NUMBER: US/09/472,087
                                                             CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR PILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 234
TYPE: PRT
ORGANISM: Homo sapiens
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Patent No. 6682736
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Best Local Similarity 69.9%
Matches 151; Conservative
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ORGANISM: Homo sapiens
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US-09-472-087-69
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Sequence 84, Application US/09453234
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                                                                                                                                                                                                                                                                                                                        PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
                                                                                                                                                                                                                                                                                                                                                                                                140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLW--VFGGGTKLTVLSRTVAAPSVF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 ARFSGSGSGTDFTLTISSLEPEDFAVYYCQ--QRNNWPLTFGGGTKVEI-KRTVAAPSVF 116
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                                                                                                                                                                                                                   4 VVTQE-SALTISPGETVTLICRSSIGAVITISNYANWVQEKPDHLFIGLIGGTNNRAPGVP 62
                                                                                                                                                                                                                                            4 VVTQESA-LITISPGETVTLICRSSIGAVTISNYANWVQEKPDHLFTGLIGGINNRAPGVP
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                                                                                                                                     Query Match
64.6%; Score 732; DB 4; Length 235;
Best Local Similarity 69.4%; Pred. No. 2.3e-64;
Matches 150; Conservative 19; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Buechler, Joe
APPLICANT: Valkirs, Gunars
APPLICANT: Valkirs, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Gray, Jeff
TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
FILE REFERENCE: 020015-000200US
FURENT APPLICATION NUMBER: US/09/456,090A
CURRENT FILING DATE: 1999-12-06
NUMBER OF SEQ ID NOS: 110
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 64.5%; Score 731.5; DB 4; Length 3
Best Local Similarity 71.4%; Pred. No. 2.5e-64;
Matches 155; Conservative 14; Mismatches 39; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-456-090A-84
; Sequence 84, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
  SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT OCANISM: Homo sapiens CTHER INFORMATION: M2-32L US-09-456-090A-84
                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                US-09-472-087-65
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US-09-453-234-84
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LENGTH: 224
                  SEQ ID NO 65
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63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLW--VFGGGTKLTVLSRTVAAPSVF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 224;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.5%; Score 731.5; DB 4; 71.4%; Pred. No. 2.5e-64;
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Fatent No. 6828121
GENERAL INFORMATION:
TITLE OF INVENTION: BACTERIAL HOST STRAINS
FILE REFERENCE: P1804R1
CURRENT RELING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US/10/011,125A
CURRENT FILING DATE: 2001-12-07
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 2
                                        APPLICANT: Valkirs, Gunars
APPLICANT: Valkirs, Gunars
APPLICANT: Lonberg, Nils
APPLICANT: Lonberg, Nils
APPLICANT: Blosite Diagnostics, Inc.
APPLICANT: Blosite Diagnostics, Inc.
APPLICANT: GenPharm International
TITLE REPRENCE: 020015-000110US
CURRENT FILING DATE: 1999-12-01
CURRENT FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 84
LENGTH: 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Sequence is synthesized.; Patent No. 6828121
US-10-011-125A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens; OTHER INFORMATION: M2-32L
US-09-453-234-84
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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Sequence 106, App Sequence 38, Appl Sequence 2, Appl Sequence 2, Appl Sequence 18, Appl Sequence 15, Appl Sequence 17, Appl

4 US-10-25-10-08A-4
5 US-10-25-10-08A-4
6 US-10-461-148-2
6 US-10-153-382-11
6 US-10-153-382-11
6 US-10-152-497-15
6 US-10-176-649-15
6 US-10-776-649-15
6 US-10-776-649-15
6 US-10-776-649-15
6 US-10-777-290-122
6 US-10-474-832-3
6 US-10-478-88-88
7 US-10-478-89-178-88-88
7 US-10-408-901-40
7 US-10-408-901-40
7 US-10-408-901-40
7 US-10-408-901-40
7 US-10-408-901-40
7 US-10-408-901-40
7 US-10-418-30-414
7 US-10-418-30-414

Sequence 1 Sequence 6 Sequence 6 Sequence

Sequence Sequence Sequence Sequence Seguence Sequence Sequence Sequence

US-10-776-649-14 US-10-776-649-65

ALIGNMENTS

Sequence 587, A Sequence 122, A Sequence 122, A Sequence 142, A Sequence 3, App Sequence 3, App Sequence 106, A

Sequence 15, P Sequence 67, P Sequence 15, P Sequence 67, P

Sequence Sequence

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RESULT 1
US-10-625-047-27
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Sequence 8, Appli
Sequence 8, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
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Sequence 28, Appl
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1 RSAVVTQESALTTSPGETVT......EVTHQGLSXPVTKSFNRGEC 218
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                                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
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US-10-625-047-28

US-10-723-003-42

US-10-150-475A-8

US-10-704-522-8

US-10-704-522-8

US-10-704-522-4

US-10-645-215-4

US-10-645-215-4

US-10-232-4

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Maximum Match 100%
Listing first 45 summaries
                                                                                                                protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Maximum DB
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1 RSAVVTQESALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPG
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95.5%; Score 1083; DB 16; Length 218;
Best Local Similarity 95.9%; Pred. No. 1.1e-84;
Matches 209; Conservative 0; Mismatches 9; Indels 0
Sequence 22-27, Application US/10625047

Sequence 27, Application US/10625047

Publication No. US20040198962A1

GENERAL INFORMATION:

APPLICANT: Meares, Claude

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: Multi-Functional Antibodies

TITLE OF INVENTION: Multi-Functional Antibodies

CURRENT APPLICATION NUMBER: US/10/625,047

CURRENT APPLICATION NUMBER: US/10/625,047

CURRENT FILING DATE: 2003-01-23

NUMBER OF SEQ ID NOS: 72

SSOTARR: PatentIN Ver. 2.1

SSOTARR: PatentIN Ver. 2.1
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ORGANISM: Artificial Sequence
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US-10-150-475A-8
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                           61 VPARFSGSLIGDKAALTIAGTQTEDEAIYFCALWYSNHWVFGGGTKLTVLSRTVAAPSVF
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Publication No. US20040254108A1
GENERAL INFORMATION:
APPLICANT: MA, Jing
APPLICANT: MA, Jing
APPLICANT: GUO, Yajun
TITLE OF INVENTION: PREPARATION AND APPLICATION OF
TITLE OF INVENTION: ANTI-TUMOR BIFUNCTIONAL FUSION PROTEINS
FILE REFERENCE: 549062000200
CURRENT APPLICATION NUMBER: US/10/723,003
CURRENT FILING DATE: 2003-11-26
                                                                                                                                                                                                                                                                                                   US-10-625-047-28

Sequence 28, Application US/10625047

Publication No. USZO040198962A1

GENERAL INFORMATION:
APPLICANT: Meares, Claude
APPLICANT: Cornellie, Todd
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Multi-Functional Antibodies
FILE REFERENCE: 023070-130910US
CURRENT FILING DATE: 2003-07-22
PRIOR APPLICATION NUMBER: US/10/625,047

PRIOR APPLICATION NUMBER: US 10/350,555

PRIOR FILING DATE: 2003-01-23
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Best Local Similarity 95.9%; Pred. No. 1.3e-84;
Matches 209; Conservative 0; Mismatches 9
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 28
LENGTH: 218
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US-10-723-003-42
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                                                                                                                                                                                                                                                                                                                                                                                                      7 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Adolf, G. et al.
TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
FILE REPRENCE: 1/1211
CURRENT APPLICATION NUMBER: US/10/150,475A
CURRENT FILING DATE: 2002-05-17
PRIOR PILING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
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PRIOR APPLICATION NUMBER: CN 2003101199300 PRIOR FILING DATE: 2003-11-25 PRIOR PPLICATION NUMBER: CN 031292909 PRIOR FILING DATE: 2003-06-13 NUMBER OF SEQ ID NOS: 68 SOFTWARE: FastSEQ for Windows Version 4.0 LENGTH: 235
                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Synthetic Construct
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 156; Conservative
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SOFTWARE: Patentin Ver.
SEQ ID NO 8
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                                              LENGTH: 213
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GENERAL INFORMATION:
APPLICANT: Adolf, Guenther:
APPLICANT: Heider, Karl-Heinz
TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
TITLE OF INVENTION: UNBER: US 0010(45,215)
CURRENT FILING DATE: AUGUST 21, 2002
PRIOR FILING DATE: AUGUST 21, 2002
PRIOR FILING DATE: AUGUST 21, 2002
PRIOR FILING DATE: AUGUST 26, 2002
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
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                                                                                                                                                                                                                  | FULLICACION NO. USAUVAULZU949A1
| GENERAL INFORMATION:
| APPLICANT: Adolf, Gunther
| APPLICANT: Baumann, Michael
| TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
| TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
| FILE REFERENCE: 1/1444
| CURRENT APPLICATION NUMBER: US 60/429,516
| PRIOR APPLICATION NUMBER: EP 02024881
| PRIOR FILING DATE: 2002-11-27
| PRIOR FILING DATE: 2002-11-08
| NUMBER OF SEQ ID NOS: 9 - 1
| SEQ ID NOS: 9 - 2.1
| SEQ ID NOS: 9 - 2.1
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                                                                                                                                                                                       Sequence 8, Application US/10704522
Publication No. US20040120949A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                   US-10-704-522-8
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                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/10150475A
; Sequence 4, Application US/20030103985A1
; GENERAL INFORMATION:
; APPLICANT: Adolf G. et al.
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
; FILE REFERENCE: 1/1211
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/307,451
; PRIOR PILING DATE: 2001-07-24
; NUMBER OF FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.2%; Score 751; DB 14; Length 213; 72.2%; Pred. No. 2.8e-56; tive 13; Mismatches 41; Indels 6
                                                                                                                         Length 213;
                                                                                                                                                                      40; Indels
                                          ; FEATURE:
; OTHER INFORMATION: Humanised Antibody BIWA 8 Light Chain
VS-10-645-215-8
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                                                                                                  66.4%; Score 753; DB 16;
Best Local Similarity 72.2%; Pred. No. 1.9e-56;
Matches 156; Conservative 14; Mismarth
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ORGANISM: Artificial Sequence
TYPE: PRT ORGANISM: Artificial Sequence
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Matches 156; Conservative
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FEATURE:
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Sequence 4, Application US/10645215

Sequence 4, Application US/10645215

Publication No. US20040126379A1

SEQUENCE 4. Application No. US20040126379A1

SETTION NO. US20040126379A1

APPLICANT: Adolf, Guenther

APPLICANT: Baum, Anke

APPLICANT: Heider, Karl-Heinz

TITLE OF INVENTION: Compositions and Methods for Treating Cancer using

TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and

TITLE OF INVENTION: Chemotherapeutic Agents

TITLE OF INVENTION: Chemotherapeutic Agents

TITLE OF INVENTION: Chemotherapeutic Agents

FILE REFERENCE: 1/1383

CURRENT FILING DATE: 2003-08-21

PRIOR PELING DATE: August 21, 2002

PRIOR PILING DATE: August 21, 2002

PRIOR FILING DATE: August 26, 2002

NUMBER OF SEQ ID NOS: 9

NUMBER OF SEQ ID NOS: 9

NUMBER OF SEQ ID NOS: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 66.2%; Score 751; DB 16; Length 213; Best Local Similarity 72.2%; Pred. No. 2.8e-56; Matches 156; Conservative 13; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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                                                    Sequence 4, Application US/10704522

Publication No. US20040120949A1

GENERAL INFORMATION:
APPLICANT: Adolf, Gunther
APPLICANT: Heider, Karl-Heinz
ITILE OF INVENTION: Compositions and methods for
ITILE OF INVENTION: Compositions and methods for
ITILE OF INVENTION: Compositions and methods for
ITILE OF INVENTION: COMPOSITION and methods for
FILE REFERENCE: 1/1414
CURRENT APPLICATION NUMBER: US/10/704,522
CURRENT FILING DATE: 2003-11-07
PRIOR APPLICATION NUMBER: US 60/429,516
FRIOR FILING DATE: 2002-11-08
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTING UNCY: 2.1
SEQ ID NO 4
LENGTH: 213
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ORGANISM: Artificial Sequence
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LENGTH: 213
                                       -10-704-522-4
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                                                                                                                                 Gaps
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; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Light Chain US-10-645-215-4
                                                                             66.2%; Score 751; DB 16; Length 213; larity 72.2%; Pred. No. 2.8e-56; Conservative 13; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.1%; Score 750; DB 9; Length 220; 71.8%; Pred. No. 3.5e-56; Live 13; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09995693
Patent No. US20020136721A1
GENERAL INFORMATION:
APPLICANT: Schwall, Ralph H.
Tabor, Kelly H.
TILE OF INVENTION: Hepatocyte Growth Factor Receptor
Antagonists and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) APPLICATION DATA: APPLICATION NUMBER: US/09/995,693 FILING DATE: 29-No. US20020136721A1-2001 CLIASSIFICATION: cUnknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0938P1
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/952,235
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 650/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 220 amino acids
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SEQUENCE CHARACTERISTICS:
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Matches 153; Conservative 1
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COMPUTER READABLE FORM:
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                                                                                                        Best Local Similarity
Matches 156; Conserv
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Sequence 4, Application US/09848832
; Publication No. US20030165507A1
; GENERAL INFORMATION:
; APPLICANT: Hooper, Douglas
; APPLICANT: Dietzschold, Bernhard
; TITLE OF INVENTION: RABIES VIRUS-SPECFIC NEUTRALIZING HUMAN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND NUCLEIC ACIDS AND RELATED METHODS
; FILE REFERENCE: HOO01.NP0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFP 123
SGSLIGDKAALTITGAQTEDBARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFPPS 125
                           DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 185
                                                                                                                 5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA
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US-10-435-299-12
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Sequence 12, Application US/10435299
Publication No. US2004005278341
GENERAL INFORMATION:
APPLICANT: Weater, George
APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
APPLICANT: Link, Brian
APPLICANT: Gingrich, Roger
APPLICANT: Gingrich, Roger
APPLICANT: Gingrich, Roger
APPLICANT: Link, Brian
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST CD3
FILE REPERENCE: 05882-0.17-6-CNUS04
CURRENT APPLICATION NUMBER: US/10/435,299
CURRENT FILING DATE: 2000-07-18
FRIOR FILING DATE: 1995-03-01
FRIOR FILING DATE: 1995-03-01
FRIOR FILING DATE: 1992-03-07
FRIOR FILING DATE: 1992-03-07
SPRIOR FILING DATE: 1992-03-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE PRECENT NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.7%; Score 745; DB 15; 71.2%; Pred. No. 9.1e-56; iive 16; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 TLSKADYEKHKVYACEVTHOGLSXPVTKSFNRGEC 218
                                                                                                                                                                                SKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                         188 SKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220
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Best Local Similarity 71.24
Matches 153; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-848-832-4
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           SALTISPGETVTLICRSSIGAVTIS - - - NYANWVQEKPDHLFTGLIGGINNRAPGVPARF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Schwall, Ralph H.
Tabor, Kelly H.
TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
Antagonists and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESONDENCE ADDRESS:
CORRESONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIDE: 94080
COMPUTER READABLE FORM:
WEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winheatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/669,971
FILING DATE: 05-Jul-2001
APPLICATION NUMBER: US/09/669,971
FILING DATE: CAUNANDATA:
APPLICATION NUMBER: US/09/669,971
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
TELLING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                   188 SKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Marschang, Diane L. REGISTRATION NUMBER: 35,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 220 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/10232408 Publication No. US20030118587A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 198
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                                                                                                                                                                                                                                                                                                                                                                                      23 VLTQSPATLSLSPGERATLACKAS---QTASRYLAWYQQKPGQAPRLLIYDTSNRATGIP 79
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Them
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                                                                                                                                                                                                                                                                     DB 10;
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                                                                                                                                                                                                                                                                     65.6%; Score 743.5; DB 1
71.8%; Pred. No. 1.4e-55;
tive 12; Mismatches 44
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71.8%; Pred. No. 1.4e-55;
iive 12; Mismatches 44
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Publication No. US20030157112A1
GENERAL INFORMATION:
APPLICANT: HOOPER, Craig
APPLICANT: DIETZSCHOLD, Bernhard
ITLE OF INVENTION: Recombinant Antibodies, and
ITLE OF INVENTION: Recombinant Antibodies, and
ITLE OF INVENTION: and Methods for Making The
FILE OF INVENTION NUMBER: US/09/848,832
PRIOR APPLICATION NUMBER: US 60/204,518
PRIOR FILING DATE: 2001-05-16
PRIOR PILING DATE: 2001-05-16
PRIOR FILING DATE: 2001-08-16
PRIOR FILING DATE: 2001-08-11
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FABUSEQ for Windows Version 4.0
CURRENT APPLICATION NUMBER: US/09/848,832
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 60/204,518
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
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Best Local Similarity 71.8<sup>1</sup>
Matches 155; Conservative
                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 71.8<sup>3</sup>
Matches 155, Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapien
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US-10-225-108A-4
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                                                                                                                                                            LENGTH: 234
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123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
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i Sequence 2, Application US/10461148

i Publication No. US20040013672A1

i CENERAL INFORMATION:

APPLICANT: Dietzschold, Bernhard

APPLICANT: HOOPEY, DOUGlas C.

ITILE OF INVENTION: RECOMBINANT ANTIBODIES AND COMPOSITIONS

ITILE OF INVENTION: AND METHODS FOR MAKING AND USING THE SAME

FILE REFERENCE: 8321-110C11-186685

CURRENT APPLICATION NUMBER: US/10/461,148

CURRENT FILING DATE: 2003-06-13

PRIOR APPLICATION NUMBER: US 60/314,023

PRIOR PILING DATE: 2001-08-21

PRIOR PILING DATE: 2001-08-21

PRIOR PILING DATE: 2001-05-04

PRIOR PILING DATE: 2001-05-04

PRIOR PILING DATE: 2000-05-16

NUMBER OF SEQ ID NOS: 24

SSOFTWARE: PREASEQ for Windows Version 4.0
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                                                                                    199 LTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 234
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US-10-461-148-2
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

June 7, 2005, 15:39:10 ; Search time 25 Seconds (without alignments) 839.010 Million cell updates/sec Run on:

US-09-671-953B-7 1134 1 RSAVVTQESALTTSPGETVT......EVTHQGLSXPVTKSFNRGEC 218 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters: 283416 segs, 96216763 residues Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	kappa chain	u	lambda chain	kappa	kappa chain	kappa	JC-kappa protein -	kappa chain	pelB leader/Ig hea	Ig kappa chain C r	Ig lambda chain V		lambda	kappa chain -	lambda chain	lambda		lambda	kappa	kappa	kappa chain	kappa	kappa chain	kappa ch	lambda-	lambda ch	lambda-2 cha	kappa	Ig kappa chain V r
ID	JE0242	JE0244	PC4156	JE0243	JE0241	A23746	S52059	S06084	PC4402	K3HU	852450	A31790	L1MS4E	S25058	806819	S06818	S20654	S06820	838865	S37484	A37927	S14237	S26653	S33161	B54256	S06822	L2MS35	868212	S68241
DB	7	7	7	N	~	~	7	~	4	Н	~	7	٦	~	7	N	7	~	7	ď	0	N	~	7	N	7	Н	7	7
Length	215	215	214	215	216	215	135	240	287	106	128	220	129	235	113	112	106	114	219	225	66	234	66	230	113	114	129	214	218
* Query Match	65.2	4.	64.2		59.8	59.3	51.0	48.5	48.3	48.0	47.7	47.1	47.0	46.4	4	4	45.9	45.3	45.1	45.1	44.9	44.5	44.4	44.3	44.1	44.0	43.9	43.9	43.9
Score	739	735	728.5	721	678.5	672	578.5	549.5	547.5	544	541	534.5	533	526	525	523.5	521	513.5	511	511	509	504.5	503	502.5	200	499.5	498	497.5	497.5
Result No.	1	8	e	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

Ig kappa chain pre	Ig kappa chain pre	monoclonal antibod	Ig kappa chain - m	Ig lambda chain V	Ig kappa chain V r	Ig lambda chain V	Ig lambda chain V	Ig lambda chain -	Ig kappa chain (mo	Ig lambda chain V	Ig lambda-1 chain	kappa	Ig lambda chain V	lambda	kappa
JL0029	S01320	JC5810	S42772	PH1089	S16112	S14582	806821	S25749	PC4203	PH1090	LIMSV	S52028	S14584	PH1088	A56169
7	7	~	7	7	~	~	0	7	~	N	-	N	~	7	0
225	234	218	217	66	219	66	113	235	219	97	116	219	66	100	210
43.7	43.7	43.4	43.2	43.1	43.0	42.9	42.9	42.8	42.7	42.2	42.2	42.2	41.7	41.7	41.4
495.5	495.5	492.5	490	488.5	488	486	486	485	484.5	478	478	478	473	473	469.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

JE0242 1g kappa chain NIG26 precursor - human Cispecies: Homo sapiens (man) Cispecies: O5-Dec-1998 #sequence revision 05-Dec-1998 #text_change 21-Jan-2000	C;Accession: JE0242 R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; St	submitted to JIPID, November 1998 A plescription: Structure relationship of kappatype light chains with AL amyloide	A;Kererence number: JEU241 A;Accession: JE0242	A;Molecule type: protein A;Residues: 1-215 <ali></ali>	C;Superfamily: immunoglobulin V region; immunoglobulin homology F:16-91/Domain: immunoglobulin homology <imm></imm>	Query Match , 65.2%; Score 739; DB 2; Length 215;	Best Local Similarity 70.4%; Pred. No. 1.4e-48; Matches 152; Conservative 17; Mismatches 43; Indels 4; Gaps 3;	Qy 4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP 62	DD 3 VLTQSPGTLSLSPGERATLSCRASQSVSNNYLAWYQQKPGQAPSLLIYDASSRATGIP 60	Qy 63 ARFSGSLIGDKAALTITGAQTEDEARYFCALMYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122	-bMI	Qy 123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182	SVTEQDSKDS
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dosis: Mul

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RESULT 2

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Use vapa chain NIG2 precursor - human C; Species: Homo sapiens (man)
C; Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C; Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C; Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
R; Alescapion: JE0244
A; Pereric number: JE0243
A; Accession: JE0244
A; Molecule type: protein
A; Molecule: protein
A; Molecule: 1-215 - ALI>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
F; 16-90/Domain: immunoglobulin homology < IMM>

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63
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PC4156
Ig lambda chain V region MabB23 - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: D-May-1996 #sequence_revision 19-Jul-1996 #text_change 21-Jan-2000
C;Accession: PC4156
R;Kwak, J.W.; Choi, B.K.; Lee, D.I.; Kang, Y.K.; Seo, Y.G.; Cho, W.K.; Han, M.H.
Gene 169, 237-239, 1996
A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a A;Reference number: PC4155
A;Accession: PC4156
A;Accession: PC4156
A;Accession: PC4156
A;Accession: PC4156
A;Accession: PC4156
A;Cross-references: GB:U28967; NID:g1262178; PIDN:AAC52488.1; PID:g1262179
C;Superfanily: Immunoglobulin V region; immunoglobulin homology
F;1-214/Product: light chain #status predicted cMAT>
F;98-110/Region: V region
F;130-198/Domain: immunoglobulin homology <IMM>
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Ig kappa chain NIG93 precursor - human
G.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C.Accession: JE0243
S.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, submitted to JIPID, November 1998
A.; Asecription: A new subgroup of k type light chains (VkV) identified in cases of A; Reference number: JE0243
A; Accession: JE0243
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                                                                                                                                                                               ARFSGSGSGTDFILTISSLOSEDFALYYCOOY--NTWPPLTFGGGTKVEI-KRTVAAPSV 116
                                                                                                                                                                                                                   FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 179
                                                                                                                                                                                                                                      ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29
                                                                         VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
                                                                                                        VLTOSPATLSVSPGERATLSCRAS -- OSVHSNLA-WYQQKPGQAPRLLIYRASTRATGIP
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                                         Gaps
                                         10;
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   Length 215;
atch 64.8%; Score 735; DB 2; Length 21: cal Similarity 71.7%; Pred. No. 2.9e-48; 157; Conservative 13; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                           SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 215
                                                                                                                                                                                                                                                                                          SSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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Query Match
Best Local S
Matches 157
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C.Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0241
R;Alin M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T
submitted to JIPID, November 1998
A;Description: Structure relationship of kappatype light chains with AL amyloidosis: Mul.
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Ig kappa chain V-III (KAU cold agglutinin) - human
C;Species de mon sapiens (man)
C;Species 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C;Accession: A23746
C;Accession: A23746
J. Siol. Chem. 266, 2836-2842, 1991
A;Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl. A;Reference number: A23746, MUID:91131575; PMID:1993660
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A;Residues: 1-216 <ALI-
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-92/Domain: immunoglobulin homology <IMM>
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>
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                                                                                                                                  Score 721; DB 2;
Pred. No. 3.2e-47;
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                                                                                                                                                                                       12; Mismatches
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70.2%;
                                                                                                                                                                                       Matches 153; Conservative
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A;Accession: JE0241
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Gaps

2

119 141

82

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pelB leader/Ig heavy chain anti-NP/linker type 205/alkaline phosphatase fusion protein c; Species: synthetic c; Species: synthetic c; Species: synthetic c; Species: synthetic c; Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 06-Nov-1998 C; Cacession: PC4402 H.; Suzuki, C.; Ueda, H.; Suzuki, E.; Nagamune, T. J. Biochem. 122, 322-329, 1997 J. Species: Construction, bacterial expression, and characterization of hapten-specific sin A; Reference number: PC4402 A; Reference number: PC4402 A; Reference number: PC4402 A; Residues: 1-287 <SUZ> C; Keywords: fusion protein
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C;Species: Homo sapiens (man)
C;Date: 3.1-Dec-1980 #sequence revision 02-Jul-1998 #text change 09-Jul-2004
C;Accession: B90562; A91651; A90806; A94417; A91639; A92047; A9242; B37927; A02116; S0
R;Gottlieb, P.D.; Cunningham, B.A.; Rutishauser, U.; Edelman, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAP---- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | : | | : | 3.06 | 1.06 | 1.06 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 14.7 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07 | 1.07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 FIFPPSDEQLKSGTASVVCLLINNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 SIFPPSTEQLATGGASVVCLMNNFYPRDISVKWKIDGTERRDGVLDSVTDQDSKDSTYSM 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 VVTQE-SALTTSPGETVTLTCRSS---IGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23. VMTQSPSSLAVSAGETVTINCKSSQSLFYSGNQKNYLAWYQQKPGQSPKLLIYWASTRQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 AVVIQESALITSPGETVILICRSSIGAVITSNYANWVQEKPDHLFTGLIGGINNRAPGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 AVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSV
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A; Molecule type: mRNA
A; Residues: 1-240 < CRO>
A; Residues: 1-240 < CRO>
A; Residues: 1-240 < CRO>
A; Cross=references: EMBL:X16129; NID:956457; PIDN:CAA34256.1; PID:956458
C; Cross=references: EmBL:X16129; NID:956457; PIDN:CAA34256.1; PID:956458
C; Reywords: heterotetramer; immunoglobulin
C; Reywords: heterotetramer; immunoglobulin
F; 1.20 Domain: ajgnal sequence #steatus predicted < SIG>
F; 21.240/Product: Ig kappa chain #status predicted < MAT>
F; 1.22.220/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                      Length 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SVFIFPPSDEQLKSG-TASVVCLLNNFYPREAKVQW-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 547.5; DB 4;
Pred. No. 4.7e-34;
                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 48.5%; Score 549.5; DB 2
Best Local Similarity 53.4%; Pred. No. 2.7e-34;
Matches 117; Conservative 24; Mismatches 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 53.4%; Pred. No. 4.7e Matches 126; Conservative 14; Mismatches
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R,Crowe, J.S.; Smitch, M.A.; Cooper, H.J.
R,Crowe, J.S.; Smitch, M.A.; Cooper, H.J.
R,Crowe, J.S.; Smitch, M.A.; Cooper, H.J.
R,Crowe, J.S.; Smitch, M.S.; Cooper, H.J.
R,Title: Nucleotide Requence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA
A,Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA
A,Reference number: S06084; MUD:90016888; PMID:2508067
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R;Frances, V.; Pandrau-Garcia, D.; Guret, C.; Ho, S.; Wang, Z.; Duvert, V.; Saeland, S. EMBO J. 13, 5937-5943, 1994
A;Title: A surrogate 15 kDa JC-kappa protein is expressed in combination with mu heavy A;Reference number: S52059; MUID:95112804; PMID:7813432
A;Accession: S52059
A;Acces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 PPSDEQLKSGTASVVGLIANFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DRFSGSGSGTDFTLTISRLEPEDFAVYYGQQYGSSPLTFGGGTKVEI-KRTVAAPSVFIF 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 VLTOSPATLSLSPGERATLSGGAS--OSVSSNYLAWYOOKPGOAPRLLIYDASSRATGIP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig kappa chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C;Accession: S06084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Species: Homo sapiens (man)
Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 08-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 KVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 VVTQESA-LITSPGETVTLICRSSIGAVTISNYANWVQEKPDHLFTGLIGGTNNRAPGVP
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                                A;Accession: A23746
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-215 < LEGO>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin preference; immunoglobulin
C;Keywords: heterocletramer; immunoglobulin
F;16-91/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                               Length 215;
                                                                                                                                                                                                                                                                                                                                                                     Query Match 59.3%; Score 672; DB 2; Length 21 Best Local Similarity 68.4%; Pred. No. 1.5e-43; Matches 147; Conservative 16; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGE 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1e-36;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 578.5;
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Best Local Similarity 89.7%;
Matches 113; Conservative
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Ig lambda chain V region - mouse
C;Species: Mus musculus (house m
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Matches 104; Conservative
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A; Residues: 1-128 <BER>
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A31790
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A TILLE: The covalent Extroction of a human gamend-temanoglobulin. VI. Amino acid sequency A MILLE: The covalent Extroction Extraction of the American Market States and States 
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A; Residues: 8-106 < KUR>
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A;Title: Chemical modification of the carboxyl groups of protein substrates enhances the A;Reference number: $02572; MUID:88005152; PMID:3115831
                                                                                                                                                                                                                       A,Map position: 2p12-2p12
C;Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;19-8M,Domain: immunoglobulin homology xIMM>
F;26-8G/Disulfide bonds: #status experimental
F;106/Disulfide bonds: interchain (to heavy chain) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Berdoz, J.; Kraehenbuhl, J.P.
submitted the EMBL Data Library, November 1994
A;Description: Specific amplification by the polymerase chain reaction of rearranged gen.
A;Reference number: S52445
A;Accession: S52450
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R.Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
R.Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
A.Title: Preliminary crystallographic data, primary sequence, and binding data for an an A;Reference number: A92686; MUID:89034213; PMID:3182835
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C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
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C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 TVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48.0%; Score 544; DB 1; Length 106; 99.1%; Pred. No. 3e-34;
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Keywords: heterotetramer; immunoglobulin
34-111/Domain: immunoglobulin homology <IMM>
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Pred. No. 6.2e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                          A,Gene: GDB:IGKC
A,Cross-references: GDB:120088; OMIM:147200
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Matches 105; Conservative
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C;Complex: Au' mmunoglobulin heterotetramer subunit consists of two identical light (ka. hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l (;Superfamily: immunoglobulin V region; immunoglobulin homology (;Keywords: heterotetramer: pyroglutamic acid F;1-19/Domain: signal sequence #status experimental <SIG>F;20-129/Domain: Ig lambda-1 chain precursor V region #status experimental <MAT>F;30-110/Modified site: pyrolidone carboxylic acid (Gln) (in mature form) #status experime: F;11-109/Disulfide bonds: #status predicted
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                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-43, TT, 45-50, G',52-58, E',60-89,'D',91-129 <BER>
A; Note: the sequence was determined from the differentiated gene
R; Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore,
Nature 298, 380-382, 182
A; Title: Somatic variants of murine immunoglobulin lambda light chains.
A; Reference number: A93282; MUID:82220143; PMID:6283385
R;Bernard, O.; Hozumi, N.; Tonegawa, S.
Cell 15, 1133-1144, 1978
A;Title: Sequences of mouse immunoglobulin light chain genes before and after somatic
A;Reference number: A90780; MUID:79084170; PMID:103630
A;Contents: H2020
A;Accession: A90780
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C;Accession: S;5058
R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, submitted to the EMBL Data Library, July 1992
A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop 8 A;Reference number: S;5057
A;Accession: S25058
A;Accession: S25058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 129;
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46.4%; Score 526; DB 2;
Best Local Similarity 50.5%; Pred. No. 1.6e-32;
Matches 109; Conservative 29; Mismatches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 533; DB 1;
Pred. No. 2.5e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 94.4%;
Matches 102; Conservative
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A;Residues: 1-235 <FIS>
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A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Contents: S43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Introns: 16/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Genetics:
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                                                               A;Molecule type: mRNA
A;Residues: 1-220 <SCH>
A;Crose-references: GS:M23626; GB:J04061; NID:g533234; PIDN:AAA39162.1; PID:g533235
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <!MM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 SIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSM 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 VMTÓSPSSLÍTVTAGEKVÍTMSCTSSOSLFNSGKOKNÝLÍWYOOKÞGOPPKVLÍYWASTRES 62
                                                                                                                                                                                                                                                                                                                                                                                                    4 VVTQE-SALTTSPGETVTLTCRSS---IGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 20-43,'N',45-70,'N',72-115,'R',117-129 <CE3>
A;Note: these proteins were isolated from serum or urine of tumor-bearing
                                                                                                                                                                                                                                                                                                                                                 Gaps
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R;Appella, E.
Proc. Natl. Acad. Sci. U.S.A. 68, 590-594, 1971
A;Title: Amino acid sequences of two mouse immunoglobulin lambda chains.
A;Reference number: A93775; MUID:71107854; PMID:5276767
A;Contents: MOPC 104E; RPC 20
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                                                                                                                                                                                                                                                                                 Length 220;
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Proc. Natl. Acad. Sci. U.S.A. 70, 2112-2116, 1973
A;Title: Mouse lambda-chain sequences.
A;Reference number: A93784; MUID:73229669; PMID:4516208
                                                                                                                                                                                                                                                                              Query Match
47.1%; Score 534.5; DB 2;
Best Local Similarity 51.6%; Pred. No. 3.4e-33;
Matches 113; Conservative 26; Mismatches 75;
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A;Residues: 'Z',21-25,'Q',27-129 <APP>
A;Accession: C93775
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Residues: 20-129 <CE2>
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A;Residues: 1-29 <BUR>
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                                         A; Accession: A31790
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RESULT 15
S06819
IG lambda chain V region (clone 10C3) - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 11-Nov-1994 #text_change 21-Jan-2000
C;Accession: 806819
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Titler Comparative sequence and immunochemical analyses of murine monoclonal anti-morg A;Reference number: 806815; MUID:90064531; PMID:255519
A;Accession: 806819
A;Accession: 806819
A;Accession: S06819
A;Accession: S06819
A;Accession: I-113 <AMLb
A;Residues: 1-113 <AMLb
C;Superfamily: Immunoglobulin V region; immunoglobulin homology
C;Keywords: heteroterramer; immunoglobulin
F;14-91/Domain: immunoglobulin homology <IMM>F;21-89/Disulfide bonds: #status predicted
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0; Gaps
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46.3%; Score 525; DB 2; Length 11:
Best Local Similarity 94.4%; Pred. No. 8.6e-33;
Matches 102; Conservative 1; Mismatches 5; Indels
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Search completed: June 7, 2005, 16:01:08 Job time: 26 secs

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P01724
Q8vde2
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P01729
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      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Q7SYU1
Q61PQ0
Q6PIQ7
Q7Z2U3
Q6GMV7
Q7Z2U7
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TISSUE-Spleen;

XX TISSUE-Spleen;

XX Streamberg R.L., Feathgold E.A., Groube L.H., Derge J.G.,

X Strausherg R.L., Feathgold E.A., Groube L.H., Derge J.G.,

X Strausherg R.L., Feathgold E.A., Schemen C.M., Schuler G.D.,

X Alausner R.D., Collins F.S., Wagner L., Wang J., Halber G.D.,

X Alausner R.D., Golden H., Moore T., Max S.L., Wang J., Halber F.,

X Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Halber F.,

X Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Halber F.,

X Hopkins R.F., Jordan H., Moore T., Max S.L., Wang M.,

X Hopkins R.F., Jordan H., Farmer A.A., Rubin G.M., Hong L.,

X Hopkins R.R., Nogwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

X Raplecon M.J., Uddin T.B., Toshiyuki, S., Carninci P., Prange C.,

X Rapla S.S., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,

X Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W.,

X Richards S., Worley K.C., Hale S., García A.M., Gay L.J., Hulyk S.W.,

X Nillalon D.K., Muzny D.M., Sodercia A.M., Gay L.J., Hulyk S.W.,

X Hilling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

X Rodriguez A.C., Grimwood J., Scheutz J., Myers R.M., Butterfield Y.S.,

X Jones S.J., Marra M.A.,

X and mouse CDNA sequences "."
                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Strausbergy R.;

Strausbergy R.;

Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

R EMBL, BC073792; AAH73792.1; -.

R InterPro; IPR003599; Ig.

R InterPro; IPR003596; Ig.

R Fam; PF07654; C1-set; 1.

R SMART; SM00407; IG; 2.

R SMART; SM00406; IG; 2.

R SMART; SM00406; IG; 1.

R SMART; SM00406; IG; 1.

R PROSITE; PS00299; IG_MKC; UNKNOWN_1.
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Last annotation update)
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ALIGNMENTS
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                                                                        ņ
                                                                                                                                                         63 ARFSGSLIGDKAALTITGAQTEDEARYFCAL---WYCNLWVFGGGTKLTVLSRTVAAPSV 119
                                                                                                                                                                                                                  FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 179
                                                                                                                                                                                                                                  137 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 196
                                                                                                                              79
                                                                                                                    80 GRFSGSGSGTEFTLSISSLQSEDFAVYFCQQYNDWL--LYTFGQGTKLEI-KRTVAAPSV
                                                                                                  4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnag.242603899;
                                            Length 235;
                                                     Se-56;
~hea 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the EMBL/GenBank/DDBJ databases
 Hypothetical protein.
SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;
                                                                                                                                                                                                                                                                         SSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                        SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235
                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
                                           DB 2;
                                        Query Match 64.6%; Score 732; DB Best Local Similarity 70.3%; Pred. No. 5e-56 Matches 154; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           235 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR003599; Ig.
Interpro; IPR007110; Ig-like.
Interpro; IPR003597; Ig cl.
Interpro; IPR003066; Ig_MHC.
Interpro; IPR003596; Ig v.
Pfam; PF07654; Cl-set; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (OCT-2001) to the
EMBL; BC016380; AAH16380.1;
HSSP; P01837; 1KCU.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Lung;
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              · SEQUENCE
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**X Tabusasplants: 242603899;

**X MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

**S trausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

**X Altachul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

**A Altachul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

**A Altachul S.F., Derdan H., Moore T., Max S.I., Wang J., Hsieh F.,

**Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

**S tapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

**Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,

**Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

**Robark S.A., McEwan P.J., McKernan R.J., Mallek J.A., Gunaratne P.H.,

**Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

**A villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

**A hiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

**A hiting M. Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

**A Richards M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

**A Jones S.J., Marra M.A.,

**A Jones S.J., Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 DRFSGSGGTDFTLTISRLEPEDFAVYYCQQYGSSQGTFGPGTKVDI-KRTVAAPSVFIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGCTKLTVLSRTVAAPSVFIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             123 PPSDEQLKSGTASVVCLLNNFYPREAKVOWKVDNALQSGNSQESVTEQDSKDSTYSLSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 VVTQESA-LTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 ;
                                                                                                                                                                                                                                                                                                                                                                                    Query Match 64.5%; Score 731; DB 2; Length 235; Best Local Similarity 69.9%; Pred. No. 6.1e-56; Matches 151; Conservative 19; Mismatches 42; Indels
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Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073191; AAH73791.1; -.
InterPro; IPR003599; IG.
InterPro; IPR007110; IG-like.
SMART; SM00409; IG; 2.
SMART; SM004015; IGc1; 1.
PRART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00239; IG_MHC; UNKNOWN_1.
SPROPHELICAL protein.
SEQUENCE 235 AA; 25520 WW; F33A145A396BA285 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 AA
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
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Homo sapiens (Human).
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Homo sapiens
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                                                                                                                                                                                                                                                      Query Match
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A Krausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Atlasher R.D., Collins F.S., Wagner L., Shammen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A plothin R.F., Jordan H., Moore T., Max. S.I., Wang J., Hsieh F.,
B. Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B. Carninci P., Forner R.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
B. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
B. Pahey J., Helton B., Ketreman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Minting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Jones S.J., Marra M.A.,
B. Marra 
                                                                                                                                                                                                                                                                                                                                                                                                                            21 RCAIQMTQSPSSLSASVGDRVTITCRASQG---ISNDLGWYQQKPGKAPKLLIYAASSLQ 77
                                                                                                                                                                                                                                                                                        1 RSAV-VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEXPDHLFTGLIGGTNNRA
                                                                                                                                                                                                                                                                                                                                                        59 PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPS
                                                                                                                                                                                                                                                      Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                        .
9
                                                                                                                                                                                                                      Length 236;
                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                      Hypothetical protein. SEGUENCE 236 AA, 25751 MW; 5BFE6A087AFAC437 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSSTLTLSKADYEKHKVYACEVTHOGLSXPVTKSFNRGEC
                                                                                                                                                                                                                    Query Match 64.2%; Score 728; DB 2; Lv
Best Local Similarity 70.0%; Pred. No. 1.1e-55;
Matches 154; Conservative 15; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                  PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PR07654; C1-set; 1.
Pfam; PR0047; ig; 2.
SMART; SM00409; IG; 2.
SMART; SM00406; IGc1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mouse cDNA sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
Homo sapiens (Human).
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TISSUB—Skeletal Muscle;

XX TISSUB—Skeletal Muscle;

XX TISSUB—Skeletal Muscle;

XX TISSUB—Skeletal Muscle;

XX Tatusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XX Tatusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

XX Altausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

XX Altschul S.F., Joedan H., Moore T., Max S.I., Wang J., Halten R.N.,

XX Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

XX Arapleton M., Goares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

XX Arapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

XX Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

XX Raha S.S., Worley N.C., McKernan K.J., Malek J.A., Gunaratne P.H.,

XX Robards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

XX Rahards S.A., Worley D.M., Sodergen B.J., Lu X., Gibbs R.A.,

XX Halting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

XX Mitting M., Touchman J.W., Green B.D., Dickson M.C.,

XX Rodriguez A.C., Grimwood J., Schnutz J., Myers R.M., Butterfield Y.S.,

XX Kzzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 RCAIRMTQSPSSFSASTGDRVTITCRAS---QSIGSYLAWYQQKPGKAPQLLIYAASTLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RSAV-VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 PGVPARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
Straugherg R.; Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases. Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BCO56256, AAH56256.1; -. HSSP; PO1034; HEZ. InterPro; IPR007110; Ig-1ike. InterPro; IPR003506; Ig-4. InterPro; IPR003596; Ig-4. InterPro; IPR003596; Ig-4. Empty PFam; PF07654; Cl-set; 1. SMART; SMO0406; IG-4. PROSITE; PS00239; IG-MHC; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                            234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSSTLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

, Score 725; DB 2;
; Pred. No. 2e-55;
19; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 68.2
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
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Altachnels S.P., Zeeberg B.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,

Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,

A phoking R.F., Jordan H., Moore T., Max S.I., Haidh F.,

A papleron M., Soares M.B., Bonaldon M.F., Casavant T.L., Scheetz T.E.,

B Erownstein M.J., Usdin T.B., Tooshiyuki S., Carnhori P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Brownstein M.J., Usdin T.B., Tooshiyuki S., Carnhori P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Norley W. Hollon B. Ketteman M., Mersh R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Marra M.A.,

"Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFP 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 VTQE-SALTISPGETVILICRSSIGAVITSNYANWVQEKPDHLFIGLIGGINNRAPGVPA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 70.2%; Pred. No. 3.4e-55;
Matches 151; Conservative 15; Mismatches 44; Indels
                                                               Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                      al protein.
236 AA; 25702 MW; 7FBFE4ED23084BC6 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.7%; Score 722.5; DB 2 70.2%; Pred. No. 3.4e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 AA
                                                                                                                                                                          InterPro; IPR007110, Ig-like.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003597; Ig_MC.
InterPro; IPR003596; Ig_WC.
Pfam; PF07654; C1-set; I.
PR003TE; PS50835; IG_LIKE; PR051TE; PS50835; IG_LIKE; IR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                           EMBL; BC005332; AAH05332.1; -. HSSP; P01834; 1HEZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mouse cDNA sequences.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
SEQUENCE FROM N.A.
TISSUE=Skeletal Muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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123 PPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSST 182
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derged J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchench C.L., Marusina K.H., Farmer A.A., Rubin G.M., Hong L.,

B Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Rownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Miting M., Madan A., Young A.C., Shevchenko Y., Bonifard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 VLTQSPGTLSLSPGERAALSCRAS--QSVNSKYLAWYQQKPGQAPRLLMYAASIRATGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 ARFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 VVTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 63.6%; Score 721; DB 2; Length 235; Best Local Similarity 69.4%; Pred. No. 4.6e-55; Matches 150; Conservative 15; Mismatches 47; Indels
                                                                                                                                                       EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 235 AA; 25646 MW; DF32B580BAD19E4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 LTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 LTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50835; IG LIKE; 2.
PROSITE; PS00290; IG MHC; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                 Submitted (JUN-2004) to the EMBL; BC073793; AAH73793.1;
                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF07654, C1-86t, T. Pfam; PF00047; 19; 2. SMART; SM00409; IG; 2. SMART; SM00407; IGC1; 1. SMART; SM00407; IGC1; 1.
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Homo sapiens (Human).
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                                                                                                                          Strausberg R.
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122

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124 PSDEQLKSGTASVVCLLANFYPRAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 LTOSPSFLSASVGDRVTITCRASOG---ISSYLAWYOOKPGKAPNLLIYAASTLOSGVPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Allschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: BCO34141; AAH34141.1; -.
HSSP; P01607; 1AR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein.
SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;
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Last annotation update)
                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 720.5; DB 2,
; Pred. No. 5.1e-55;
15; Mismatches 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC
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InterPro; IPR001359; IG.
InterPro; IPR007110; IG-11ke.
InterPro; IPR003597; IG_C1.
InterPro; IPR003597; IG_C1.
InterPro; IPR003596; IG_WHC.
InterPro; IPR003596; IG_WHC.
InterPro; IPR004596; IG_V.
SWART; SW00409; IG; 2.
SWART; SW00409; IG; 2.
PR0SITE; PS00290; IG_LIKE; 2.
PROSITE; PS00290; IG_LIKE; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 151; Conservative
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Homo sapiens (Human).
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                                                                                                                                                                                                                                                                  TISSUE=Lung;
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Q6P5S8
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Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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Brownstein M.J., Ugdin T.B., Toshlyuki S., Carninci P., Prange C.,
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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 VTOE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVOEKPDHLFTGLIGGTNNRAPGVPA
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 236;
                                                                                                                                                                                     Straubberg R.;
Submitted (UJN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC073763; AAH77363.1; -.
R InterPro; IPR001599; IG-
R InterPro; IPR001599; IG-
R InterPro; IPR001599; IG-
R InterPro; IPR001599; IG-
R InterPro; IPR001596; IG-
R InterPro; IPR001596; IG-
R InterPro; IPR001596; IG-
R InterPro; IPR001596; IG-
R Pfam; PPF00647; IG-
R Pfam; PF00047; IG-
R SMART; SM00406; IG-
R SMART; SM00406; IG-
R PROSITE; PS50835; IG-
R PROSITE; PS50835; IG-
R PROSITE; PS50835; IG-
M Hypothetical procein.
C SEQUENCE 236 AA; 25924 MW; FDE2093DC560CFF7 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.5%; Score 720.5; DB 2; 69.3%; Pred. No. 5.1e-55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149; Conservative 17; Mismatches
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                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
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Homo sapiens (Human).
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Matches 149; Conserv
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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Villalon D.K., Muray D.M., Sodergren E.J., Lu K., Gabbs R.A.,
Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,
Jones S.J., Marra M.J.,
Jones S.J., Marra M.A.,
Jones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236 AA; 25773 MW; 953E37BEB4FF5F27 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                             and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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69.6%; Pred. No. 6.3e-55;
iive 17; Mismatches 44
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PROSITE; PS00290; IG MHC; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=Glandular pool- thyroid;
                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003599; IG.
InterPro; IPR003109; IG-like.
InterPro; IPR003597; Ig-c1.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003596; Ig-v.
Pfam; PF07654; C1-8et; I.
SMART; SM00409; IG; 2
                                                                                                                                                                                                                                                                                                                                                                                         EMBL; BC062704; AAH62704.1;
HSSP; P01837; 1KCU.
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Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00407; IGC1; 1.
SMART; SM00406; IGV; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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SEQUENCE FROM N.A. TISSUE=Brain;

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A Straubberg R.L., Feingold E.A., Grouse C.H., Derge J.G.,

A Klausner R.D., Collins F.S., Wagner L., Schaefer C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

A popting R.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B capleton M., Soares M.B., Bonaldo M.F., Caarainci P., Prange C.,

Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,

B Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Carcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Radan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B akesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S.J., Marra M.A.;

T "Generation and initial analysis of more than 15,000 full-length human

Et Proc. Natl. Acad. Sci. U.S.A., 99:16899-16903(2002).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Mypothetical protein.
Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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EMBL, BC032451; AAH32451.1; -.
HSSP, P01837; 1KCU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEQUENCE 236 AA; 25834 MW; 6647A9E77A3C0053 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 TLTLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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Best Local Similarity 69.6%; Pred. No. 9.4e-55;
Matches 151; Conservative 18; Mismatches 43
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PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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InterPro; IPR003100; Ig-like.
InterPro; IPR003100; Ig_C1.
InterPro; IPR003506; Ig_MHC.
InterPro; IPR003596; Ig_WHC.
Pfam; PP07654; C1-8et; I.
SMART; SM00407; IGC1; I.
SMART; SM00407; IGC1; I.
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WEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A trausDerg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
A trachul S.F., Zeeberg B. B., Buerow K.H., Schaefer C.R., Schuler G.D.,
A trachul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
A dechul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
A physins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brapleron M., Soares M.B., Bonaldo M.E., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
W. Villalon D.K., Muray D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Willialon D.K., Muray D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Willialon D.K., Muray D.M., Sodergren B.J., Lu X., Gibbs R.A.,
W. Halton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
M. Hakealey R. W., Touchman J.W., Green B.D., Dickson M.C.,
A Dlakealey R. W., Touchman J.W., Green B.D., Dickson M.C.,
A Chancardion and initial analysis of more than 15,000 full-length human
A mouse C.DNA sequences.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFP
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Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC03775; AAH7375.1; -.
InterPro; IPR003159; Ig.
InterPro; IPR003159; Ig.
InterPro; IPR003059; Ig.
InterPro; IPR00306; Ig.MHC.
InterPro; IPR003066; Ig.V.
Pfam; PF07654; Cl-set; I.
EMART; SM00409; IG; 2.
SMART; SM00409; IG; 2.
SMART; SM00406; IGv; 1.
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
REQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;
                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.0%; Score 714.5; DB 2;
69.3%; Pred. No. 1.7e-54;
ive 16; Mismatches 45;
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PROSITE; PS00290; IG MHC; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 69.39
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                             FROM N.A.
                                            SEQUENCE FROM N.A.
                    NCBI_TaxID=9606;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Klausherrimary B-Cellis;
A Klausherrimary B-Cellis
Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Klausher R.D., Collins F.S., Wagner L., Shennen C.W., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marushna K., Farmer A.A., Rubin G.M., Hong L.,
Brapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Weßwan P.J., McKernan K.J., Mallek J.A., Gunaratne P.H.,
Bosak S.A., McKernan F.J., McKernan R.J., Mullahy S.J.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Hilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Halesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rozywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A Jones S.J., Marra M.A.;
A Green E.D., Myers R.M., Butterfield Y.S.,
A Halesley M. A., Wanners M.A.;
A Jones S.J., Marra M.A.;
A Green E.D., Dickson M.C.,
A Jones S.J., Marra M.A.;
A Green E.D., Dickson M.C.,
A Jones S.J., Marra M.A.;
A Green E.D., Dickson M.C.,
A Jones S.J., Marra M.A.;
A Green E.D., Dickson M.C.,
A Jones S.J., Marra M.A.;
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                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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REMBL, BC073764; AA473764.1; -...

RINEEPRO; IPR007110; Ig-11ke.

RINEEPRO; IPR003599; Ig-21.

RINEEPRO; IPR003596; Ig-4.

RINEEPRO; IPR003596; Ig-4.

REMART; SM00409; IG; 2.

REMART; SM00409; IG; 2.

REMART; SM00406; IG; 2.

REMART; SM00406; IG; 2.

REMART; SM00406; IG; 1.

REMART; SM00406; IG; 2.

REMART; SM00406; IG; 1.

REMOSITE; PS00290; IG_MRC; UNKNOWN_1.
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SEQUENCE 236 AA, 25707 MW, 4FC8E14B6559EFC9 CRC64;
27, Last sequence update)
27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Matches 148; Conservative 19; Mismatches
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TISSUE=Primary B-Cells;
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                                                                         Hypothetical protein.
Homo sapiens (Human).
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                                                                                                                                                                                                                            NCBI_TaxID=9606;
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05-JUL-2004 (TrEMBLrel. 27, Created)

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                                                                                                                                                                                                                                    MEDLINE=228825; PubMed=12477932; DOI=10.1073/pnas.242603899; MEDLINE=228825; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Altschul S.F., Zeeberg B. Buecow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B. Buecow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heish F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brapleton M., Judin T.B., Toshiyuki S., Carninci P., Prange C., Asaba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Nilalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A., Willalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Abraheley R.W., Touchman J.W., Green B.D., Dickson M.C., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., R., Green S.J., Marra M.A., Shalska D., Smailus D.E., Schnerch A., Schein J.E., Marra M.A., Touchman J. W., Green E.D., Dickson M.C., Marra M.A., M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 RFSGSLIGDKAALTITGAQTEDEARYFCALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFP 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 PSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 MTQSPSTLSASVGDRVTIACRAS---QWISDWLAWYQQKPGKAPKLLIYDASRLESGVPS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 VTQE-SALTTSPGETVTLTCRSSIGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 RFSGSGSGTEFSLTISGLQPDDFATYYCQPYNSNSPQFGQGTKVEI-KRTVAAPSVFIFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC034146; AAH34146.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25871 MW; BE01A28CD06EEE26 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.3%; Score 706.5; DB 2
68.8%; Pred. No. 8.7e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 68.8%; Pred. No. 8.7e-5
Matches 148; Conservative 18; Mismatches
                                236 AA
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SMART; SMO0407; IG21; 1.
SMART; SMO0406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS02290; IG_MHC; UNKNOWN_1.
HYPOCHELICAL PYCLEIN
SEQUENCE 236 AA; 25871 MW; BE01A;
                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003597; Ig c1.
InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig v.
Pfam; PF07654; C1-6et; I.
                                                            05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences."
                               PRELIMINARY;
                                                                                                                   Hypothetical protein.
                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                      NCBI_TaxID=9606;
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RESULT 13
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A Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Rausner R.D., Colling F.S., Wagner L.H., Derge J.G.,
Altachul S.F., Zeeberg B. Buerow K.H., Schmen C.M., Schuler G.D.,
Altachul S.F., Zeeberg B. Buerow K.H., Schmefer C.F., Bhate N.K.,
RA Hopking R.F., Jordan H., Moore T., Max S.I., Wang J., Hohe F.
A stapleton M., Soares M.B., Bonaldo M.F., Casrainci P., Prange C.,
RA Brownstein M.J., Uddin T.B., Tochiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Robak S.A., McEwan P.J., McKernan R.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley W.C., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley W.C., Shevchenko Y., Bouffard G.G.,
Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Dones S.J., Marra M.A.,
Rodriguez A.M., Saleka U., Smailus D.E., Schnerch A., Schein J.E.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield H.M. Mannan M.M. Mannan M.M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 RCAIQLTQSPSSLSASVGERVTITCRASQG---ISSALAWYQQKPGKPPKLLIYDASTWE 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCC29444; AAH29444.1; -.
HSSP; PO1607; IAR2.
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236 AA; 25741 MW; BD50AF071FBEB351 CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
184 TLSKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
                                               202 TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236
                                                                                                                                                                                                                                                                                                                      236 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; itensolation 19.
InterPro; IPR00310; ig-like.
InterPro; IPR003059; ig-like.
InterPro; IPR0030596; ig-MHC.
InterPro; IPR003596; ig-NHC.
InterPro; IPR004059; ig-N-Pfam; PF00564; cl-ect; ig-NHC.
SMART; SM00409; ig; 2.
SMART; SM00407; igcl; 1.
SMART; SM00407; igcl; 1.
PROSITE; PS00290; ig ILKE; 2.
PROSITE; PS00290; ig MHC; UNKNOWN_1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dest Local Similarity os.or
Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro, IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004
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119 VFIFPPSDEQLKSGTASVVCLLANNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 178
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI _TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.3%; Score 695; DB 2; Length 240; 69.0%; Pred. No. 9e-53; ive 17; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC034142; AAH34142.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 AA; 26234 MW; 188D4DD8BB781EC4 CRC64;
                                   05-JUL_2004 (TrEMBLrel. 27, Created)
05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                      240 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMARY; SM00409; IG; 2.
SMARY; SM00409; IGC1; 1.
SMARY; SM00406; IGC1; 1.
PROSITE; PSS0835; IG LIKB; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR005130, 19-1ike.
InterPro; IPR001597, 19_C1.
InterPro; IPR003597, 19_C1.
InterPro; IPR003596, 19_MHC.
InterPro; IPR003596, 19_V.
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                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=Lung;
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10 ALTISPGETVILICESSIGAVTIS--NYANWVQEKPDHLFTGLIGGTNNRAPGVPARFSG :|::||| ::||| :::||| || ||| ||||

Best Local Similarity 69.09 Matches 147; Conservative

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DEQLKSGTASVVCLLANNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTL 185
                                SLIGDKAALTITGAQTEDEARYFC--ALWYCNLWVFGGGTKLTVLSRTVAAPSVFIFPPS 125
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                                                                                                                                                                       186 SKADYEKHKVYACEVTHQGLSXPVTKSFNRGEC 218
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